

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 03:01:23 ; Search time 4588 seconds

(without alignments)
10762.406 Million cell updates/sec

Title: US-09-901-556C-1

Perfect score: 1207

Sequence: 1 accggcgccctgaacca.....agtcgtgtgctgcaggtag 1207

Scoring table:

IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	1207	100.0	2703	6	A79612
6	1207	100.0	2703	6	AR091289
7	1207	100.0	2703	6	E12603
8	1207	100.0	2703	6	E14291
9	1207	100.0	2703	6	E15606
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ALIGNMENTS

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DEFINITION Sequence 1 from patent US 6197550.
ACCESSION AR137664
VERSION AR137664.1 GI:14479173
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1207)
AUTHORS Hotten,G., Neidhardt,H., Bechtold,R. and Pohl,J.
TITLE DNA sequences encoding growth/differentiation
JOURNAL Patent: US 6197550-A 1 06-MAR-2001;
FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 5, 3e-218;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS Sequence 1 from Patent WO9504819.
DEFINITION A43194
ACCESSION A43194
VERSION A43194.1 GI:2298567
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 2703)
AUTHORS Hoellen,G., Neidhardt,H. and Paulista,M.
TITLE NEW GROWTH/DIFFERENTIATION FACTOR OF THE TGF- $\beta$ (b) FAMILY
JOURNAL BIOHARM GBS ZUR BIOTECHNOLOGI (DB)
PATENT: WO 9504819-A, 1, 16-Feb-1995;
OTHER PUBLICATION CA 2169171, 950216
OTHER PUBLICATION ZA 9405992, 950314
OTHER PUBLICATION AU 7498694, 950228
OTHER PUBLICATION DE 4420157, 950223.
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Best Local Similarity 100.0%; Pred. No. 4, 5e-218;
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 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE
 AUTHORS Hoeften, G., Pohl, J., Bechtold, R., Paulista, Michael and Unsicker, K.
 TITLE USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE NERVOUS SYSTEM
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RESULT 4

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LOCUS A60247 2703 bp DNA linear PAT 06-MAR-1998
DEFINITION Sequence 1 from Patent WO9706254.
ACCESSION A60247.1 GI:3715254
VERSION A60247.1 GI:3715254
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Kimura,M., Matsumoto,T., Takahashi,M., Kawal,S. and Fujino,Y.
TITLE HUMAN MP52 ARG PROTEIN
JOURNAL Patent: WO 9706254-A 1 20-FEB-1997;
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Query Match 100.0%; Score 1207; DB 6; Length 2703;
Best Local Similarity 100.0%; Pred. No. 4,5e-218;
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Db 1359 GATCTTGGGAAGAGCCCTGGAGACAGGCGCAAGCAGCGGCCCCCGAGAGGCGGCGC 1418
OY 481 TGCCCACTGAAGCTGTGCAAGTGGCCAGGCGCGGCGAGCGGCGCTCTGTGTGTGTGTGT 540
Db 1419 TGCCCACTGAAGCTGTGCAAGTGGCCAGGCGCGGCGAGCGGCGCTCTGTGTGTGTGTGT 1478
OY 541 GCGCTCGTGCACAGGCTGTGACGATGTGGGTGGAGGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 1479 GCGCTCGTGCACAGGCTGTGACGATGTGGGTGGAGGTGTGTGTGTGTGTGTGTGTGTGT 1538
OY 601 CCGAAACCTTTAAGAACTCGGCCCGCAGCTGTGCTGGAGAGTGTTCGACATCTGGAAAGCTCTT 660
Db 1539 CCGAAACCTTTAAGAACTCGGCCCGCAGCTGTGCTGGAGAGTGTTCGACATCTGGAAAGCTCTT 1598
OY 661 GCGGCTGACCTCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 720
Db 1599 GCGGCTGACCTCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1658
OY 721 CCGTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 1659 CCGTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1718
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Db 1719 CCGCTTGGCCAGAGACGATAGACCGTGTATGAGTACCTGTTCAGCCGACGGCAAAACG 1778
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QY 1201 CAGGTAG 1207
Db 2139 CAGGTAG 2145

RESULT 5
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LOCUS Definition Sequence 2 from Patent WO9723612.
ACCESSION A79612
VERSION A79612.1 GI:6092582
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 2703)
AUTHORS Hoelten,G. and Bechthold,R.
TITLE TARGETED COMPOUNDS WITH CARTILAGE FORMATION-INDUCING AND/OR BONE
FORMATION-INDUCING ACTIVITY
JOURNAL Patent: WO 9723612-A 2 03-JUL-1997;
BIOPH BIOTECH ENTW PHARM GMBH (DE); HOETTEN GERTRUD (DE)
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 602 a 758 c 784 g 559 t
ORIGIN

Query Match 100.0%; Score 1207; DB 6; Length 2703;
Best Local Similarity 100.0%; Pred. No. 4,5e-218;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GACTGTGACCCCAAAAGAGAGCTTCCGAGGAGCAAGGACACCCCAAAAGAGAGTCTGT 120
Db 999 GACTGTGACCCCAAAAGAGAGCTTCCGAGGAGCAAGGACACCCCAAAAGAGAGTCTGT 1058
QY 121 CCCCAGTCTCTTCTGTGTAAGAGGCGAGGAGCCCGGGCCCCACAGAGAGCCCAAGGA 180
Db 1059 CCCCAGTCTCTTCTGTGTAAGAGGCGAGGAGCCCGGGCCCCACAGAGAGCCCAAGGA 1118
QY 181 GCCGTTGGCCACCACCCCAATCACACCCCAAGTACATGCTTCGCTGTACAGAGAGCT 240

Db 1119 GCGGTTGGCCACCCCCCAATCACACCCCAAGTACATGCTTCGCTGTACAGAGAGCT 1178
QY 241 GTCCGATGCTACAGAAAGGAGGACAGAGCGTGAAGTTGGAGGCTGGCCAA 300
Db 1179 GTCCGATGCTACAGAAAGGAGGACAGAGCGTGAAGTTGGAGGCTGGCCAA 1238
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QY 781 CCGCTGGCCAGGACGATTAAGACCGTGTATGAGTACCTGTTCACGCGGCGGCAAAAGC 840
Db 1719 CCGCTGGCCAGGACGATTAAGACCGTGTATGAGTACCTGTTCACGCGGCGGCAAAAGC 1778
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QY 961 ACCCTTGAGTACGAGGCTTCCACTGGAGGGGCTGTGGAGTCCCATTCGCTGCCA 1020
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Db 2019 CACACACCAACCACTGCTGTGTGCCCCAGCGGCTGAGTCCCATCAGACATCTCTTCATGTA 2078
QY 1141 CTCTGCCAACAACGCTGTATAGCAGTATGAGACATGGTCTGGAGTGTGTGGCTG 1200
Db 2079 CTCTGCCAACAACGCTGTATAGCAGTATGAGACATGGTCTGGAGTGTGTGGCTG 2138
QY 1201 CAGGTAG 1207
Db 2139 CAGGTAG 2145

RESULT 6

Thu Aug 28 08:27:30 2003

us-09-901-556c-1.rge

Page 6

AR091289	AR091289	2703 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	Sequence 1 from patent US 5994094.				
DEFINITION	AR091289				
ACCESSION	AR091289.1	GI:10018044			
VERSION					
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2703)				
AUTHORS	Hotten G., Neishardt, H. and Paulista, M.				
TITLE	Growth/differentiation factor of the TGF-.beta. family				
JOURNAL	Patent: US 5994094-A 1 30-NOV-1999;				
FEATURES	location/Qualifiers				
source	1..2703				
	/organism="unknown"				
BASE COUNT	602 a 758 c 784 g 559 t				
ORIGIN					

Query Match	100.0%;	Score 1207;	DB 6;	Length 2703;
Best Local Similarity	100.0%;	Pred. No. 4.5e-218;		
Matches 1207; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Db	939	ACGGGGGGCCCTGTAACCAACCGACGACACCCGCCCAACCAAGGACAGCTACAGGCCG	998
OY	61	GACTGTAACCCCAAAAGGACGCTCCCGGAGGCAAGGACCCCAAAAGGATCTCT	120
Db	999	GACTGTAACCCCAAAAGGACGCTCCCGGAGGCAAGGACCCCAAAAGGATCTCTGT	1058
OY	121	CCCGACGCTCTTCTGCTGAAAGAAAGCCAGGAGACCCGGGCCCAAGAGACCCCAAGA	180
Db	1059	CCCGACGCTCTTCTGCTGAAAGAAAGCCAGGAGACCCGGGGCCCCAAGAGACCCCAAGA	1118
OY	181	GCCGTGTGCCACCCCCCATCACACCCACAGATATGATCTCTGCTGTACAGACACT	240
Db	1119	GCCGTGTGCCACCCCCCATCACACCCACAGATATGATCTCTGCTGTACAGACACT	1178
OY	241	GTCGCATGCTGACAAAGGAGGACACACACGTAAGTTGGAGGCTGCTGGCCAA	300
Db	1179	GTCGCATGCTGACAAAGGAGGACACACACGTAAGTTGGAGGCTGCTGGCCAA	1238
OY	301	CACCATACACACTTATTGACAAAGGACAAAGTACCCGAGTCCGTGTACAGAACCA	360
Db	1239	CACCATACACACTTATTGACAAAGGACAAAGTACCCGAGTCCGTGTACAGAACCA	1298
OY	361	GAGGTACAGTGTGATTAATGAGCCCTGGAGAAAGATGGGCTGTGCGGGGCGACTGCG	420
Db	1299	GAGGTACAGTGTGATTAATGAGCCCTGGAGAAAGATGGGCTGTGCGGGGCGACTGCG	1358
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OY	481	TGCGCAGTGAAAGCTGTCCAGCTCCACCGGCGCGGACCGGCGCTCCTCTTGATGATG	540
Db	1419	TGCGCAGTGAAAGCTGTCCAGCTCCACCGGCGCGGACCGGCGCTCCTCTTGATGATG	1478
OY	541	GGCGTCCGAGCGCTGACGAGATGTGCTGGAGAGTTCGATGTGGAAACCTCTT	600
Db	1479	GGCGTCCGAGCGCTGACGAGATGTGCTGGAGAGTTCGATGTGGAAACCTCTT	1538
OY	601	CGAATCTTAAGAACTGGCGCCAGCTGTGCTCGAGATCGAGAGCCTGGGAAACGGGGAG	660
Db	1539	CGAATCTTAAGAACTGGCGCCAGCTGTGCTCGAGATCGAGAGCCTGGGAAACGGGGAG	1598
OY	661	GGCGCTGGACCTCCGTGGGCTTGAGCCGCGCCCGCGAGGTCCACGAGAGAGC	720
Db	1599	GGCGCTGGACCTCCGTGGGCTTGAGCCGCGCCCGCGAGGTCCACGAGAGAGC	1658
OY	721	CGTGTCTCGTGTGTGTGGCGGACCAAGAAACGGGACCTGTCTTAAATGAGATTAAAGC	780

Db	165	CCGTCCTCCGTCGTCCTTTGGCCGCCACCCAGAAAGAAAGGAGACCTGTCCTTTAAATGACATTTAAAGC	1718
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Db	1719	CCGCTCTGGCCAGAGACATTAAGACCCGTGTATGATACCTGTTAGCCAGCGCGAAACG	1778
QY	841	GGGGGCCCCACTGGCCACTGCGCCAGGCGAAGCCGACCAGCAAGACCTTAAAGCTCGTG	900
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QY	901	CAGTCGGAAGGACATGCATGTCTCACTTCAAGAGACATGGCTGGGACGATGGATATGCG	960
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Db	2079	CTCTGGCAACAAAGTGGTGTATTAAGCAGTATGAGGACATGGCTGTGGAACTCGTGGGCTG	2138
QY	1201	CAGGTAG 1207	
Db	2139	CAGGTAG 2145	

RESULT 7
F13603

LOCUS	2703 bp	DNA	linear	PAT 27-APR-1998
DEFINITION	E12663			
CDNA encoding new protein	HMW (high molecular weight)	human	MP52.	
Accession	E12663			

VERSION E12603.1 GI:3251435
KEYWORDS JP 1997031098-A/1.
SOURCE Homo sapiens (human)

REFERENCE

1 (bases 1 to 2703)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS KIMURA, M., MATSUMOTO, I., TAKAHASHI, M., KAWAI, S. and FUJINO, Y.
TITLE NEW PROTEIN HMW HUMAN MP52
JOURNAL Patent: JP 1997031098-A 1 04-FEB-1997;
HOECHST JAPAN LTD

COMMENT
OS Homo sapiens (human)
PN JP 1997031098-A/1
PD 04-FEB-1997
PF 24-JUL-1995 JP 1995218022

PI KIMUDA MICHIO, MATSUMOTO TOMOAKI, TAKAHASHI MIKIKO, PI KAWAI SHINJI,
PI FUJINO YUKIO
DC 007414/47 261W38/00 261W38/00 261W38/00 012W57/00 DC

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C12P21/02/C12N5/10,  
PC (C12P21/02,C12R1:91);  
CC strandedness: Double;  
GC GC content: 50.00%;
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key	Location/Qualifiers
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BASE COUNT 602 a 758 c 784 g 559 t

ORIGIN

Query Match 100.0%; Score 1207; DB 6; Length 2703;
Best Local Similarity 100.0%; Pred. No. 4,5e-218;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGGGGGGCCCTTAACCCCAAGGAGACACCTCCCAAAACAGGAGGCTACAGCCCG 60
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QY 61 GACTGTGACCCCAAGAGACAGCTTCCCGAGGAGGACACCCCAAAAGAGAGATCTGT 120
DB GACTGTGACCCCAAGAGACAGCTTCCCGAGGAGGACACCCCAAAAGAGAGATCTGT 1058
QY 121 CCCCAGCTCTCTTCTGTGAAGAGGCGAGGAGCCCGGCCCCACAGAGCCCAAGGA 180
DB CCCCAGCTCTCTTCTGTGAAGAGGCGAGGAGCCCGGCCCCACAGAGCCCAAGGA 1118
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QY 1201 CAGGTAG 1207
DB CAGGTAG 2139

RESULT 8
LOCUS E14291 2703 bp DNA linear PAT 28-JUL-1999
DEFINITION DNA encoding human MP52.
ACCESSION E14291
VERSION E14291.1 GI:5708974
KEYWORDS JP 1997295945-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2703)
AUTHORS Takahashi, M., Makishima, F. and Kimura, M.
TITLE PRODUCTION OF MATURE TYPE BONE INDUCING FACTOR
JOURNAL Patent: JP 1997295945-A 6 18-NOV-1997;
HOECHST YAKUHIN KOGYO KK
OS Homo sapiens (human)
PN JP 1997295945-A/6
PD 18-NOV-1997
PI 30-APR-1996 JP 1996130618
PI TAKAHASHI MIKIO, MAKISHIMA FUSAO, KIMURA MICHIO PC
AG1K38/22.C07K14/52.C12N9/64.C12N15/09.C12P21/02.C12P21/06. PC
(C12N9/64.
PC C12R1:91).(C12P21/02.C12R1:91);
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CC topology: Linear;
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BASE COUNT 602 a 758 c 784 g 559 t

ORIGIN

us-09-901-556c-1.rge

Page 8

	Query Match	100.0%	Score 1207; DB 6;	Length 2703;
	Best Local Similarity	100.0%;	Pred. NO. 4.5e-218;	
	Matches 1207; Conservativity			

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	CP 1998080273-A/3.							Homo sapiens					
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	Kitajawa,H., Jitsukawa,T., Nakagawa,H. and Yanagisawa,S.							Monoecious, Antlbody FOR MP52					
	Patent JP 1998080273-A 3 31-MAR-1998;							HOCHST YAKUHIN KOGYO KK					
	OS Homosapiens (human)							PN JP 1998080273-A/3					
	PD 01-MAR-1999							PE 01-MAR-1999 JP 1997131631					
	PR 13-MAY-1998							PI KITAGAWA HIROSHI, JITSUKAWA TOMOFUMI, NAKAGAWA HIROSHI, PI					
	PC YAMAGISHIMA SACHIKO							C12N15/02,C07H21/04,C07K16/22,C12N5/10,C12P21/00,C12P21/08, PC					
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LOCUS HSDGF5 2703 bp DNA linear PRI 24-FEB-1995
 DEFINITION H.sapiens Gdf5 gene.

ACCESSION

X80915.1 GI:671524
 GDF-5 gene; TGF-beta superfamily.

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

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BASE COUNT 602 a 758 c 784 g 559 t
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IMAGE:5243109, mRNA, complete cds.
ACCESSION BC032495
KEYWORDS MGC.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2643)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, Bethesda, MD 20892-2590,
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.

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REMARK USA
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: mgc@nci.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (ILNL)
Sequencing Center (NISC),
Gaithersburg, Maryland:
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nci.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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Young, A., Zhang, L.-H. and Green, E.D.
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through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAX Plate: 64 Row: P Column: 24
This clone was selected for full length sequencing because it
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Thu Aug 28 08:27:30 2003

us-09-901-556c-1.rpt

Page 12

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VERSION AX083552.1 GI:13185362
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REFERENCE Hoeten, G., Bechtold, R. and Pohl, J.
AUTHORS 1
TITLE Monomelic protein of the tgf- β (b) family
JOURNAL Patient MO 011041-A 1 15-FEB-2001;
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GenCore version 5.1.6
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(without alignments)
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SUMMARIES

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Human TGF-beta MP5
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Growth differentia
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Nucleotide sequenc
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Human bone Inducin
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Human brain expres
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Probe #6432 for ge
Probe #8105 used t
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PI Hoelten G, Neidhardt H;
XX MPI: 1993-272824/34.
DR P-FSDB; MAR0800.
XX
PT New transforming growth factor-beta family proteins and DNA -
PT in tissue and wound repair, in treatment of bone, cartilage
XX and tooth defects, and antibodies for diagnosis
PS
XX Claim 3; Page 17; 29pp; English.
PS
CC The sequences given in AAQ47709-10 represent embryo and liver derived
CC human transforming growth factor-beta (TGF-beta) genes respectively.
CC The proteins encoded by these sequences may be used in a pharmaceutical
CC composition for the treatment of various bone, cartilage or tooth
CC defects and in tissue and wound repair processes. These proteins
CC may also be used as immunosuppressors in organ transplants and in
CC cosmetic surgery. Antibodies raised against these proteins may be
CC used for diagnostic purposes.
CC (updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 1207 BP; 254 A; 383 C; 371 G; 199 T; 0 other;

Query Match 100.0%; Score 1207; DB 149; Length 1207;
Best Local Similarity 100.0%; Pred. No. 3.2e-249;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 ACCGGGCGGCGCCGGAACCCCAACGACACCCCTCCCAACCAAGCGAGCTACAGCCCG 60
Db 1 ACCGGGCGGCGCCTGAACCCCAACGACACACCCCTCCCAACCAAGCGAGCTACAGCCCG 60
0Y 61 GACTGTGACCCCAAGGACGCTTCCGGAGGCAAGGACCCCAAGCAAGAGATCTGT 120
Db 61 GACTGTGACCCCAAGGACGCTTCCGGAGGCAAGGACCCCAAGCAAGAGATCTGT 120
0Y 121 CCCGAGCTCTCTTCGCTGAAGAAAGGACGAGAGAGCCCGGCCCCACGAGAGCCCAAGA 180
Db 121 CCCGAGCTCTCTTCGCTGAAGAAAGGACGAGAGAGCCCGGCCCCACGAGAGCCCAAGA 180
0Y 181 GCGGTTTGGCCCAACCCCGCATACACCCCAAGATCACTGCTCTGCTGACAGAGAGCT 240
Db 181 GCGGTTTGGCCCAACCCCGCATACACCCCAAGATCACTGCTCTGCTGACAGAGAGCT 240
0Y 241 GTCCGATCTCTACAGAAAGGAGGACACAGCAGCTGAAGTTGGAGGCTGCGTCGCCAA 300
Db 241 GTCCGATCTCTACAGAAAGGAGGACACAGCAGCTGAAGTTGGAGGCTGCGTCGCCAA 300
0Y 301 CACCATCACCAAGCTTTATTGCAAAAGGCAAGATGACCGAGTCCCTGTGTCAAGAGCA 360
Db 301 CACCATCACCAAGCTTTATTGCAAAAGGCAAGATGACCGAGTCCCTGTGTCAAGAGCA 360
0Y 361 GAGGTAGCTGTTTACATTATAGTGCCCTGGAGAAAGATGAGGAGCTCATGAGGAGCGAG 420
Db 361 GAGGTAGCTGTTTACATTATAGTGCCCTGGAGAAAGATGAGGAGCTCATGAGGAGCGAG 420
0Y 421 GATCTTCGGAGAAAGCCCTCGGACAGGCGCAAGCGAGCGGCCCGCGAGGCGGAGCGGCG 480
Db 421 GATCTTCGGAGAAAGCCCTCGGACAGGCGCAAGCGAGCGGCCCGCGAGGCGGAGCGGCG 480
0Y 481 TGCCAGACTGAAGCTGTCCAGCTGCCCCAGCGCGCGGCGAGCGGCGCTCTTGCTGATGT 540
Db 481 TGCCAGACTGAAGCTGTCCAGCTGCCCCAGCGCGCGGCGAGCGGCGCTCTTGCTGATGT 540
0Y 541 GCGCTCGGTCGAGGCGCTGAGCAGATCTGCTGGAGAGGTTTGCATATCGGAAGCTCTT 600
Db 541 GCGCTCGGTCGAGGCGCTGAGCAGATCTGCTGGAGAGGTTTGCATATCGGAAGCTCTT 600
0Y 601 CCGAAATTTAAGAACTCGGCGGAGTGAGCTGAGAGCTGAGAGGCTGGGAACGGGCGAG 660
Db 601 CCGAAATTTAAGAACTCGGCGGAGTGAGCTGAGAGCTGAGAGGCTGGGAACGGGCGAG 660
0Y 661 GGGCGGTGAGACTCTCGTGGGCTGGGCTTTCAGACCGCGCGCGGAGGTCCAGAGAAAGGC 720
Db 661 GGGCGGTGAGACTCTCGTGGGCTGGGCTTTCAGACCGCGCGCGGAGGTCCAGAGAAAGGC 720

[illegible]

Thu Aug 28 08:27:31 2003

us-09-901-556c-1.rng

Page 4

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XX 30-APR-1996; 96UP-0130618.
PR
XX
XX (FARH ) HOECHST YAKUHIN KOGYO KK.
XX PA (FARH ) HOECHST PHARM & CHEM KK.
XX
XX
XX Kimura M, Makishima F, Takahashi M;
XX
XX WPI; 1997-549748/50.
DR
XX
XX P-PSDB; AAM36100.
XX
XX
XX Production of mature bone morphogenetic protein - by treatment of
XX PT precursor protein with a processing enzyme such as furin either
XX PT directly or by expressing them both in the same host
XX
XX
XX
XX
XX Example 1; Pages 21-25; 34pp; Japanese.
XX
XX
XX The present sequence encodes MP52, which is a bone morphogenetic
XX CC protein (BMP).
XX CC
XX CC Mature BMP can be produced by directly adding a BMP processing
XX CC enzyme to a solution containing BMP precursor protein, or by
XX CC transforming an animal cell with expression vectors containing DNA
XX CC encoding the enzyme and precursor protein, culturing the
XX CC transformant and isolating the mature BMP from the culture. The
XX CC method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7,
XX CC which can be used to treat bone formation or regeneration
XX CC abnormalities.
XX
XX Sequence 2703 BP; 602 A; 759 C; 783 G; 559 T; 0 other;

```

Query Match	100.0%;	Score 1207;	DB 18;	Length 2703;
Best Local Similarity	100.0%;	Pred. No. 3,6e-249;		
Matches 1207;	Conservative	0;	Mismatches	0;
		Indels	0;	Gaps
OY	1	ACGGGGGGGGCCCTGMAACCCAGCCAGACACCCCTCCCCCAACAAAGGACAGCTACAGCCG	60	
Db	939	ACGGGGGGGGCCCTGMAACCCAGCCAGACACCCCTCCCCCAACAAAGGACAGCTACAGCCG	998	
OY	61	GACTGTGACCCCAAAAGACAGCTCTCCGGAGGCAAGCACCCCCCAAAAGCAGATCTGT	120	
Db	999	GACTGTGACCCCAAAAGACAGCTCTCCGGAGGCAAGCACCCCCCAAAAGCAGATCTGT	1058	
OY	121	CCCCAGCTCTTCTGCTGTGAAGAAAGGCCAGGGAGCCCGGGCCCCCAAGAGCCCAAGSA	180	
Db	1059	CCCCAGCTCTTCTGCTGTGAAGAAAGGCCAGGGAGCCCGGGCCCCCAAGAGCCCAAGSA	1118	
OY	181	GCCGTTTGCACCACCCCATCATCACACCCACGATATACATCTCTCCCTTACAGACGCT	240	
Db	1119	GCCGTTTGCACCACCCCATCATCACACCCACGATATACATCTCTCCCTTACAGACGCT	1178	
OY	241	GTCGAGTGTGACAGAAAGGAGGCAACAGCAGGCTGAATTTGGAAGGCTGGGCTGGCCAA	300	
Db	1179	GTCGAGTGTGACAGAAAGGAGGCAACAGCAGGCTGAATTTGGAAGGCTGGGCTGGCCAA	1238	
OY	301	CACCATCACCACTTATTTGACAAAGGGCAAGTACCAGAGTCCCTGTGTACAGAAACA	360	
Db	1239	CACCATCACCACTTATTTGACAAAGGGCAAGTACCAGAGTCCCTGTGTACAGAAACA	1298	
OY	361	GAGGTACGTGTTTGACATTTAGTCCCTTGAGAAAGATGGGCTGTGGGGCCAGACTGG	420	
Db	1299	GAGGTACGTGTTTGACATTTAGTCCCTTGAGAAAGATGGGCTGTGGGGCCAGACTGG	1358	
OY	421	GATCTTTCGGAAGAAAGCCCTCGAGACAGGCAACGACGAGCCCCCGGAGAGGCGGAGC	480	
Db	1359	GATCTTTCGGAAGAAAGCCCTCGAGACAGGCAACGACGAGCCCCCGGAGAGGCGGAGC	1418	
OY	481	TGGCCACAGCTGAAGCTGTCAAGTGTGCCAGGCGGCGGCAAGCGGCTCTCTGTGAGATG	540	
Db	1419	TGGCCACAGCTGAAGCTGTCAAGTGTGCCAGGCGGCGGCAAGCGGCTCTCTGTGAGATG	1478	
OY	541	GGCGTCCGTGCACAGGCTGTGACGATCTGGCTGTGGAGATGTTGACATCTGGAACTCTT	600	
Db	1479	GGCGTCCGTGCACAGGCTGTGACGATCTGGCTGTGGAGATGTTGACATCTGGAACTCTT	1538	

OY	60	CGAACCCTTAAAGAACTGGGGCCAGAGCTGTGGCTGGAGCTGGAGGCTGGCAACGGGGGAG	660
Db	1539	CGAACCCTTAAAGAACTGGGGCCAGAGCTGTGGCTGGAGCTGGAGGCTGGCAACGGGGGAG	1539
OY	661	GGCGGTGGACATCCGCTGGCCCTGGGCTTGCACCGCGCGCCCGGCAAGTCCACAGAAAGC	720
Db	1599	GGCGGTGGACATCCGCTGGCCCTGGGCTTGCACCGCGCGCCCGGCAAGTCCACAGAAAGC	1598
OY	721	CGTGTCTCGTGTGTGGCGCGCACCCAGAAACGGGACCTGTCTTAAATGAGATTAAAGC	780
Db	1659	CGTGTCTCGTGTGTGTGGCGCGCACCCAGAAACGGGACCTGTCTTAAATGAGATTAAAGC	1718
OY	781	CGCGCTGTGGCCAGAGCATTAAGACCGGTGTATGAGTACTGTGTTCAGCCAGCGGCGAAACG	840
Db	1719	CGCGCTGTGGCCAGAGCATTAAGACCGGTGTATGAGTACTGTGTTCAGCCAGCGGCGAAACG	1778
OY	841	GGCGGGCCCACTGGCCACTGCGCCAGGGCAGCGACCCAGCAAGAACCTTAAAGGTCGCTG	900
Db	1779	GGCGGGCCCACTGGCCACTGCGCCAGGGCAGCGACCCAGCAAGAACCTTAAAGGTCGCTG	1838
OY	901	CAGTGGGAAGGCACTGCATGTCAACTTCCAGAGACATGGGTGGGAGCACTGGATCATGCG	960
Db	1839	CAGTGGGAAGGCACTGCATGTCAACTTCCAGAGACATGGGTGGGAGCACTGGATCATGCG	1898
OY	961	ACCCCTTGAGTACGAGGCTTTCACACTGGAGGGGCTGTGGAGTTCCTATGGCGGCCCA	1020
Db	1899	ACCCCTTGAGTACGAGGCTTTCACACTGGAGGGGCTGTGGAGTTCCTATGGCGGCCCA	1958
OY	1021	CGTGGAGCCCAAGAAATCATGCAGTCAATCCAGACCTGTGATGAACTCCATGGACCCCGAGTC	1080
Db	1959	CGTGGAGCCCAAGAAATCATGCAGTCAATCCAGACCTGTGATGAACTCCATGGACCCCGAGTC	2018
OY	1081	CACACGACCACCTGTGTGTGTGCCACGCGGGCTGAGTCCCATCAGCAGATCTCTTCAATTGA	1140
Db	2019	CACACGACCACCTGTGTGTGTGCCACGCGGGCTGAGTCCCATCAGCAGATCTCTTCAATTGA	2078
OY	1141	CTCTGCGCAACAACGTGTGTATTAAGCAGTATGAGAGACATGTCGTGGAGTCTGTGGCTG	1200
Db	2079	CTCTGCGCAACAACGTGTGTATTAAGCAGTATGAGAGACATGTCGTGGAGTCTGTGGCTG	2138
OY	1201	CAGGTAG 1207	
Db	2139	CAGGTAG 2145	
RESULT 4			
AAT69695			
ID	AAT69695 standard; DNA; 2703 BP.		
AC	AAT69695:		
XX			
DI	04-MAR-1998 (first entry)		
XX			
DE	DNA encoding human TGF-beta protein MP52.		
XX			
KW	Human transforming growth factor-beta; TGF-beta; superfamily; cartilage; bone inducing activity; inhibic; bone resorption; ss.		
XX			
OS	Homo sapiens.		
XX			
FH			
FT	Key		
FT	CDS		
FT			
XX			
PN	DE19548476-A1.		
XX			
PD	26-JUN-1997.		
XX			
PF	22-DEC-1995; 95DE-1048476.		
XX			
PR	22-DEC-1995; 95DE-1048476.		

PA (FARH) HOECHST PHARM & CHEM KK.
 XX Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M.
 PI WPI: 1997-132636/12.
 XX P-PSDB; AAT61412.
 DR
 XX
 PT High molecular weight human MP52 growth or differentiation factor -
 PT promotes bone induction, is useful for treatment and prevention of
 PT bone disease
 XX
 XX
 PS Claim 1: Page 12-16; 25pp; Japanese.
 XX
 XX AAT61412 encodes a high mol. wt. form of a human growth/differentiation
 CC factor MP52. MP52 promotes bone induction and is useful for plastic
 CC reconstructive surgery, cosmetic facial treatment, bone transplantation
 CC and tooth implantation. It is also useful for the treatment and
 CC prevention of disorders of bone formation, bone, cartilage, joint
 CC tissue, skin, mucous membranes, nails or teeth; for wound treatment and
 CC tissue regeneration; and for the treatment of skeletal disorders and
 CC fractures.
 XX
 XX
 SO Sequence 2703 BP; 602 A; 758 C; 784 G; 559 T; 0 other;
 Query Match 100.0%; Score 1207; DB 18; Length 2703;
 Best Local Similarity 100.0%; Pred. No. 3.6e-249;
 Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCGGGGGCGCCCTGAACCCAGCCAGACACCCCTCCCAACAGAGGCTACAGCCCG 60
 DB 939 ACCGGGGGCGCCCTGAACCCAGCCAGACACCCCTCCCAACAGAGGCTACAGCCCG 998
 QY 61 GACTGTGACCCCAAAAGAGACGCTTCCGGAGGCAAGCACCCCAAAAGCAGATCTGT 120
 DB 999 GACTGTGACCCCAAAAGAGACGCTTCCGGAGGCAAGCACCCCAAAAGCAGATCTGT 1058
 QY 121 CCCAGACTCTCTCTGCTGTAAGAGAGGCGAGGAGCCGGGCCCCAGACAGAGCCAGAGA 180
 DB 1059 CCCAGACTCTCTCTGCTGTAAGAGAGGCGAGGAGCCGGGCCCCAGACAGAGCCAGAGA 1118
 QY 181 GCGCTTTCGCCACCCGCCCATCACAACCCAGAGTACATGCTGTGCTACAGAGAGCT 240
 DB 1119 GCGCTTTCGCCACCCGCCCATCACAACCCAGAGTACATGCTGTGCTACAGAGAGCT 1118
 QY 241 GTCCGATGCTGACAGAAAGAGGAGCAAGAGCGCTGAAGTGAAGGCTGGCGCCGCA 300
 DB 1179 GTCCGATGCTGACAGAAAGAGGAGCAAGAGCGCTGAAGTGAAGGCTGGCGCCGCA 1238
 QY 301 CACCATCACCAGCTTATTATGACAAAGGCGAAGATACCGAGGTCCTGGTCAAGAGCA 360
 DB 1239 CACCATCACCAGCTTATTATGACAAAGGCGAAGATACCGAGGTCCTGGTCAAGAGCA 1298
 QY 361 GAGGTACGTTGTGACATTAGTCCCTGAGAGAGATGGGCTGTGGGGCCGAGACTCG 420
 DB 1299 GAGGTACGTTGTGACATTAGTCCCTGAGAGAGATGGGCTGTGGGGCCGAGACTCG 1358
 QY 421 GATCTTGGCGAAGAACCCCTCGAGACAGGCGCAAGCAGCGGCCCGGAGAGCGGGCGG 480
 DB 1359 GATCTTGGCGAAGAACCCCTCGAGACAGGCGCAAGCAGCGGCCCGGAGAGCGGGCGG 1418
 QY 481 TGCCGAGCTGAAGCTGTCCAGCTGCGCCAGCGCGGCGAGCGGCTCTCTTGCTGAGAT 540
 DB 1419 TGCCGAGCTGAAGCTGTCCAGCTGCGCCAGCGCGGCGAGCGGCTCTCTTGCTGAGAT 1478
 QY 541 GCGCTTCGTCGCAAGGCTGAGAGGATTCGGCTGGAGGCTGTCGATCTGGAAGCTCTT 600
 DB 1479 GCGCTTCGTCGCAAGGCTGAGAGGATTCGGCTGGAGGCTGTCGATCTGGAAGCTCTT 1538
 QY 601 CCGAATCTTTAAGAACTCGGCCAGCTGTGCTGAGCTGAGAGGCTGGGAACGGGGCAG 660
 DB 1539 CCGAATCTTTAAGAACTCGGCCAGCTGTGCTGAGCTGAGAGGCTGGGAACGGGGCAG 1598
 QY 661 GCGCGTGAGACTTCGCTGGCTGGGCTTGACCGCGCGCCGCGAGGTCCAGAGAAAGC 720

DB 1599 GCGCGTGAGACTTCGCTGGCTGGGCTTGACCGGCCCGCGAGGTCCAGAGAAAGC 1658
 QY 721 CCGTTCGTCGTCGTTGTTGGCGCCAGCAAGAAACGAGCTGTTCTTTAATGATTAAGC 780
 DB 1659 CCGTTCGTCGTCGTTGTTGGCGCCAGCAAGAAACGAGCTGTTCTTTAATGATTAAGC 1718
 QY 781 CCGCTGTGCGCAGAGCATTAAGACCGTGTATGATACCTGTTCAGCCAGCGGCAAAAGC 840
 DB 1719 CCGCTGTGCGCAGAGCATTAAGACCGTGTATGATACCTGTTCAGCCAGCGGCAAAAGC 1778
 QY 841 GCGGGCCCACTGCGCACTGCGCAGAGGCAAGGCGACCGCAAGAACTTAAGCTCGCTG 900
 DB 1779 GCGGGCCCACTGCGCACTGCGCAGAGGCAAGGCGACCGCAAGAACTTAAGCTCGCTG 1838
 QY 901 CAGTCGAAGGCACTGATGATCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 960
 DB 1839 CAGTCGAAGGCACTGATGATCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 1898
 QY 961 ACCCTTGATGACGAGGCTTTCAGTGGAGGAGGCTGTGCGAGTTCCATTGCGCTGCA 1020
 DB 1899 ACCCTTGATGACGAGGCTTTCAGTGGAGGAGGCTGTGCGAGTTCCATTGCGCTGCA 1958
 QY 1021 CCGGAGCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 DB 1959 CCGGAGCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2018
 QY 1081 CACACCAACCACCTGTGTGTGTCGACGCGGCTGATCCATCAGATCTCTTCATTGA 1140
 DB 2019 CACACCAACCACCTGTGTGTGTCGACGCGGCTGATCCATCAGATCTCTTCATTGA 2078
 QY 1141 CTCTGCCCAACAGTGTGTATATAGAGTATAGAGACATGTGTGTGTGTGTGTGTGT 1200
 DB 2079 CTCTGCCCAACAGTGTGTATATAGAGTATAGAGACATGTGTGTGTGTGTGTGTGT 2138
 QY 1201 CAGGTAG 1207
 DB 2139 CAGGTAG 2145
 RESULT 6
 ID AAT59405 standard; DNA; 2703 BP.
 AC AAT59405:
 DT 15-OCT-1997 (first entry)
 XX
 XX DNA encoding human MP52 protein.
 DE
 XX Human; MP52; transforming growth factor; TGF; beta; medicament;
 KW treatment; prevention; nervous system; disease; neuropathology;
 KW aging; ds.
 XX
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 640..2145
 FT /tag= a
 FT /product= MP52
 PN DE19525416-AL.
 XX
 PD 16-JAN-1997.
 XX
 PD 12-JUL-1995; 95DE-1025416.
 PF
 XX 12-JUL-1995; 95DE-1025416.
 PR
 XX
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 XX Bechold R, Hoelten G, Paulista M, Pohl J, Unsicker K;
 PI

PI Jitsukawa T, Kitagawa H, Nakagawa H, Yanagisawa S;
XX WPI: 1998-008877/01.
DR P-PSDB; AAM33008.
XX
XX Mouse anti-human MP52 monoclonal antibody - recognises the dimeric
PT form of MP52 but not the monomer, and does not cross-react with
PT TGF-beta or BMP-2
XX
XX Disclosure; Pages 31-35; 46pp; Japanese.
XX
XX The present sequence, which encodes human MP52, was used in the
CC preparation of a novel mouse monoclonal antibody (Mab), which
CC recognises dimeric but not monomeric human MP52. The Mab has a
CC heavy chain of subclass gamma, and does not cross-react with
CC TGF-beta or BMP-2. The Mab may be used to purify and assay human
CC MP52, especially recombinant MP52.
XX
SQ Sequence 2703 BP; 602 A; 758 C; 784 G; 559 T; 0 other:

Query Match 100.0%; Score 1207; DB 19; Length 2703;
Best Local Similarity 100.0%; Pred. No. 3,6e-249;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACCGGGGGCGCCCTTAACCAAGCAGACACCTCCCAACAAAGCAGCTACACCCG 60
DB 939 ACCGGGGGCGCCCTTAACCAAGCAGACACCTCCCAACAAAGCAGCTACACCCG 998
OY 61 GACGTGACCCCAAGAGACAGCTCCCGAGGCAAGGCAACCCCAAGCAGATCTGT 120
DB 999 GACGTGACCCCAAGAGACAGCTCCCGAGGCAAGGCAACCCCAAGCAGATCTGT 1058
OY 121 CCCAGGCTCTCTCTGTGAAGAGGCGCAGGAGCCCGGGCCCGCAGAGAGCCCAAGA 180
DB 1059 CCCAGGCTCTCTCTGTGAAGAGGCGCAGGAGCCCGGGCCCGCAGAGAGCCCAAGA 1118
OY 181 GCCGTTTGGCCACCCCATCACACCCAGATACATGCTCTGCTGTACAGAGCGCT 240
DB 1119 GCCGTTTGGCCACCCCATCACACCCAGATACATGCTCTGCTGTACAGAGCGCT 1178
OY 241 GTCCGATGCTGACAAAGAGGAGCAACAGCAGCGTGAAGTTGAGAGCGTGGCCAA 300
DB 1179 GTCCGATGCTGACAAAGAGGAGCAACAGCAGCGTGAAGTTGAGAGCGTGGCCAA 1238
OY 301 CACCATCACAGCTTTATTGACAAAGGCAAGATGACGAGTCCCGTGTACAGAAACA 360
DB 1239 CACCATCACAGCTTTATTGACAAAGGCAAGATGACGAGTCCCGTGTACAGAAACA 1298
OY 361 GAGGTACGTTTACATTAAGTCCCTGAGAGAGATGGCTGCTGGGGCCGAGCTGCG 420
DB 1299 GAGGTACGTTTACATTAAGTCCCTGAGAGAGATGGCTGCTGGGGCCGAGCTGCG 1358
OY 421 GATCTTGGGAGAAAGCCCTGAGACAGGCGCAAGCCCGCCCGAGGCGGGGCGC 480
DB 1359 GATCTTGGGAGAAAGCCCTGAGACAGGCGCAAGCCCGCCCGAGGCGGGGCGC 1418
OY 481 TGCCACAGTGAAGCTGTCAAGCTGCCAGCGCGCGGAGCGCGGCTCTTGTGATGT 540
DB 1419 TGCCACAGTGAAGCTGTCAAGCTGCCAGCGCGCGGAGCGCGGCTCTTGTGATGT 1478
OY 541 GCGCTCGGTGCGAGCGCTGAGAGGATGCTGGAGAGTGTTCACATCTGGAAGCTCTT 600
DB 1479 GCGCTCGGTGCGAGCGCTGAGAGGATGCTGGAGAGTGTTCACATCTGGAAGCTCTT 1538
OY 601 CCGAAGCTTTAAGAACTCGGCGCAGCTGCTGCGAGAGTGAAGGCTGGGAACGGGAG 660
DB 1539 CCGAAGCTTTAAGAACTCGGCGCAGCTGCTGCGAGAGTGAAGGCTGGGAACGGGAG 1598
OY 661 GCGCGTGAAGCTCGGTGGCTGTGAGACCGGCGCGCGGAGAGTCCACGAGAAAGC 720
DB 1599 GCGCGTGAAGCTCGGTGGCTGTGAGACCGGCGCGCGGAGAGTCCACGAGAAAGC 1658
OY 721 CCGTGTCTGCTGCTGTTTGGCGGACCAAGAAAGGAGACCTGTTCTTAATGAGATTAGGC 780

DB 1659 CCTGTCTGCTGTTTGGCCGACCAAGAAAGGAGACCTGTTCTTAATGAGATTAGGC 1718
OY 781 CCGCTGTGCGCAGGACGATTAAGACGCTGTATGAGTACCTGTTTCAAGCGCGGAAAGC 840
DB 1719 CCGCTGTGCGCAGGACGATTAAGACGCTGTATGAGTACCTGTTTCAAGCGCGGAAAGC 1778
OY 841 GCGGGCCCGACCTGGCCACTGCGCAGAGGCGAGCCAGCAAGAACTTAAGGCTGCTG 900
DB 1779 GCGGGCCCGACCTGGCCACTGCGCAGAGGCGAGCCAGCAAGAACTTAAGGCTGCTG 1838
OY 901 CAGTCGGAAGGACATGCTGATGCACTTCAAGACATGGGCTGGGACGACTGATCATCCG 960
DB 1839 CAGTCGGAAGGACATGCTGATGCACTTCAAGACATGGGCTGGGACGACTGATCATCCG 1898
OY 961 ACCCTTGAAGACAGGCTTCCACTGCGAGGCGGTGCGAGTTCCATGCGCTGCCA 1020
DB 1899 ACCCTTGAAGACAGGCTTCCACTGCGAGGCGGTGCGAGTTCCATGCGCTGCCA 1958
OY 1021 CCTGAGCCGACGATCATGCAAGTCAACACCTGATGAATCATGACCCGAGTC 1080
DB 1959 CCTGAGCCGACGATCATGCAAGTCAACACCTGATGAATCATGACCCGAGTC 2018
OY 1081 CACACCAACCCAGCTGCTGTGTGCCAGCGGCTGAGTCCATACATCTCTTATTTGA 1140
DB 2019 CACACCAACCCAGCTGCTGTGTGCCAGCGGCTGAGTCCATACATCTCTTATTTGA 2078
OY 1141 CTCTGCCAACAAGCTGTATTAAGCAGTATGAGACATGCTGCGAGTGTGGCTG 1200
DB 2079 CTCTGCCAACAAGCTGTATTAAGCAGTATGAGACATGCTGCGAGTGTGGCTG 2138
OY 1201 CAGGTAG 1207
DB 2139 CAGGTAG 2145

RESULT 9
AB088242
ID AB088242 standard; cDNA; 2703 BP.
XX
XX AB088242;
XX
XX 18-SEP-2002 (first entry)
DE
XX Human osteoblast differentiation related cDNA SEQ ID NO 149.
KW Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW osteoporosis; osteopathia; ss.
XX
XX Homo sapiens.
OS
XX
XX W0200250301-A2.
PN
XX
XX 27-JUN-2002.
PD
XX
XX 18-DEC-2001; 2001WO-US48276.
PE
XX
XX 18-DEC-2000; 2000US-255882P.
PR 24-APR-2001; 2001US-285691P.
XX
XX (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
XX
XX JI D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
PI Metzl L;
XX
XX WPI: 2002-557663/59.
DR
XX
XX Use of genes and their expression profiles associated with osteoblast
PT differentiation for screening modulators bone formation, for diagnosis
PT or treating e.g. osteoporosis, or as markers for the differentiation
PT process
XX

PS Claim 1; SEQ ID NO 149; 78bp + Sequence Listing; English.

CC The invention relates to genes and their expression profiles are used
CC for:
CC (a) screening modulators of precursor stem cell differentiation into
CC osteoblasts, or bone tissue deposition;
CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
CC osteoblast formation or osteoporosis; or
CC (c) treating or monitoring treatment of the conditions cited in (b), or
CC monitoring the progression of bone tissue deposition.
CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
CC drug-induced abnormalities in bone formation or bone loss, conditions
CC that involve altered bone metabolism (e.g. idiopathic juvenile
CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
CC osteoblast differentiation associated cDNA marker of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 2703 BP; 602 A; 758 C; 784 G; 559 T; 0 other;

Query Match	100.0%;	Score 1207;	DB 24;	Length 2703;
Best Local Similarity	100.0%;	Pred. No. 3.6e-249;		
Matches 1207; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	ACGGGGGGGGCCCTGAACCCCAAGCCAGACACCCCTCCCAACAAGGACAGCTACAGCCG	60
Db	939	ACGGGGGGGGCCCTGAACCCCAAGCCAGACACCCCTCCCAACAAGGACAGCTACAGCCG	998
OY	61	GACTGTGACCCCAAAAGGACAGCTTCCGGAGGCGAAGGCAACCCCAAAAGCAGATCTGT	120
Db	999	GACTGTGACCCCAAAAGGACAGCTTCCGGAGGCGAAGGCAACCCCAAAAGCAGATCTGT	1055
OY	121	CGCGACTCTCTTCTGCTGGAAGAAAGCCAGGGAACCCGGGCCCTCACAGAGCCCAAGGA	180
Db	1059	CGCGACTCTCTTCTGCTGGAAGAAAGCCAGGGAACCCGGGCCCTCACAGAGCCCAAGGA	1118
OY	181	GCCGTTTGGCCACCCGCCCATCACAACCCACAGATACATCTCTGCTGTACAGACGT	240
Db	1119	GCCGTTTGGCCACCCGCCCATCACAACCCACAGATACATCTCTGCTGTACAGACGT	1117
OY	241	GTCCGATGCTGACAAAGAGGAGGCACAGCAGGTAACTGTGAGCTGGCTGGCCAA	300
Db	1179	GTCCGATGCTGACAAAGAGGAGGCACAGCAGGTAACTGTGAGAGCTGGCTGGCCAA	1238
OY	301	CACCATCACACACTTATTATGACAAAGGCGAAGTACCGAGTCCGCTGTCAGAAAGA	360
Db	1239	CACCATCACACACTTATTATGACAAAGGCGAAGTACCGAGTCCGCTGTCAGAAAGA	1298
OY	361	GAGGTACGTTGTGACATTAGTGCCTCGAGAAAGATGGGCTCTGGGGGCGAGCTGGG	420
Db	1299	GAGGTACGTTGTGACATTAGTGCCTCGAGAAAGATGGGCTCTGGGGGCGAGCTGGG	1358
OY	421	GATCTTGGGGAAAGAGCCCTGCGACAGCGGCACAGCCCGCGGAGGCGGGCGGC	480
Db	1359	GATCTTGGGGAAAGAGCCCTGCGACAGCGGCACAGCCCGCGGAGGCGGGCGGC	1418
OY	481	TGGCCAGCTGAAGCTGTGCTCAGCTGTCCGACAGCGGCGACCGGGCTCTCTGCTGAATGT	540
Db	1419	TGGCCAGCTGAAGCTGTGCTCAGCTGTCCGACAGCGGCGACCGGGCTCTCTGCTGAATGT	1478
OY	541	GGCGTCCGTGCGAGGCTGTGACAGGATGTGGCTGGGAGTGTGACATCTGGAAGCTCTT	600
Db	1479	GGCGTCCGTGCGAGGCTGTGACAGGATGTGGCTGGGAGTGTGACATCTGGAAGCTCTT	1538
OY	601	CGGAACCTTAAAGAACTGGGCCACAGCTGTGCTTGAAGCTGGAAGCTGGGAACGGAGCAG	660
Db	1539	CGGAACCTTAAAGAACTGGGCCACAGCTGTGCTTGAAGCTGGAAGCTGGGAACGGAGCAG	1598
OY	661	GGCGGAGGACCTCGCTGGCTGGGGCTTCGACCGCGCGCCCGGACAGTCCACAGAAAGCG	720

Dd	1599	GGGCGTGGACCTCCGTGGGCTTCGACC	CGGCCGCGGCAGAGTCCACGAAAGC	1658
Oy	721	CCGTGTCCCGTGTTTGGCCGACCAAGA	AACGGGACCTGTTTAATGAAATTAAAGC	780
Dd	1659	CGTGTTCCTGGTGTGTGGCCGACCA	GAAGAACGGGACTGTCTTTAATGAAATTAAAGC	1718
Oy	781	CGGCTCTGGCCAGAGCATTAAGACCG	TGTATGACTGTTCAGCCAGCGGCGAAAAC	840
Dd	1719	CGGCTCTGGCCAGAGCATTAAGACCG	TGTATGACTGTTCAGCCAGCGGCGAAAAC	1778
Oy	841	GGGGGCCCCACTGGCCCACTGGCCCA	CGGCGCAACCGCACCCAGCAAGAACCTTAAGGCTCGCTG	900
Dd	1779	GGGGGCCCCACTGGCCCACTGGCCCA	CGGCGCAACCGCACCCAGCAAGAACCTTAAGGCTCGCTG	1838
Oy	901	CAGTCGGAAGCACTGCATGTCAACTTC	CAAGGACATGGGCTGGGAGCACTGGATCATACGC	960
Dd	1839	CAGTCGGAAGCACTGCATGTCAACTTC	CAAGGACATGGGCTGGGAGCACTGGATCATACGC	1898
Oy	961	ACCCCTTGGAGTAGAGGCTTTCACACT	CGAGGGGCTGTGGAGTCCCATTTGCGCTCCA	1020
Dd	1899	ACCCCTTGGAGTAGAGGCTTTCACACT	CGAGGGGCTGTGGAGTCCCATTTGCGCTCCA	1958
Oy	1021	CCGTGAGCCCAAGATCATGACAGTCA	GCAGACCCCTGATGAATCCATGAGACCCGAGATC	1080
Dd	1959	CCGTGAGCCCAAGATCATGACAGTCA	GCAGACCCCTGATGAATCCATGAGACCCGAGATC	2018
Oy	1081	CACACACCCACCTGCTGTGTGGCCAG	CGGGCTGAGTCCCATCAGACATCCCTTCATTTGA	1140
Dd	2019	CACACACCCACCTGCTGTGTGGCCAG	CGGGCTGAGTCCCATCAGACATCCCTTCATTTGA	2078
Oy	1141	CTGTGCAACAACGTGTGTATAAGCAG	TATGAGACATGATGTCGTGGAGTGGTGGCTG	1200
Dd	2079	CTGTGCAACAACGTGTGTATAAGCAG	TATGAGACATGATGTCGTGGAGTGGTGGCTG	2138
Oy	1201	CAGGTAG	1207	
Dd	2139	CAGGTAG	2145	
<hr/>				
RESULT 10				
AAQ96209	ID	AAQ96209 standard; DNA; 1207 BP.		
XX	XX	AAQ96209;		
XX	XX	25-MAR-2003 (updated)		
AC	DT	23-NOV-1995 (first entry)		
XX	XX	Murine protein MP52.		
DE	DE	Bone morphogenetic protein; MP52; tendon; Ligament; ss.		
KW	XX	Mus musculus.		
OS	OS	Key	Location/Qualifiers	
FH	FT	CDS	845..1204	
ET	XX	/tag-a		
XX	PN	W09516035-A2.		
XX	PD	15-JUN-1995.		
PF	XX	06-DEC-1994; 94WO-US14030.		
XX	XX	02-NOV-1994; 94US-0333576.		
PR	PR	07-DEC-1993; 93US-0164103.		
XX	PR	25-MAR-1994; 94US-0217780.		
PA	PA	(GENY) GENETICS INST INC.		
XX	XX	(HARD.) HARVARD COLLEGE.		
XX	XX	Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolman NM;		
XX	XX	Wozyne JM;		

XX WPI: 1995-224320/29.
DR P-PSDB; AAR78731.
XX Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
PT compsn. for inducing tendon/ligament-like tissue formation
XX Example: Page 51-52; 84pp; English.

XX Oligos #6 and #7 (AA096218 & AA096219) are used as primers for the
CC amplification of a 275 bp DNA probe, the internal 269 bp of which
CC corresp. to nts #607 to #865 of AA096207, from the BMP-12 encoding
CC plasmid subclone PCR1-12. This probe was radioactively labeled
CC and used to screen a murine genomic library. DNA sequence analysis
CC of one of positively hybridizing recombinants named MVR23 indicates
CC that it encodes a portion of the mouse gene corresp. to the PCR
CC product m93 (murine homolog of the MP-52 sequence AA096209/R78731).
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 1207 BP; 254 A; 384 C; 370 G; 199 T; 0 other:

Query Match 99.9%; Score 1205.4; DB 16; Length 1207;
Best Local Similarity 99.9%; Pred. No. 7e-249;
Matches 1206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ACCGGGGGCGCCCTGAAACCAAGAGACACCTCCCAACAAAGAGAGCTACAGCCCG 60
1 ACCGGGGGCGCCCTGAAACCAAGAGAGACACCTCCCAACAAAGAGAGCTACAGCCCG 60
61 GACGTGACCCCAAAAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
61 GACGTGACCCCAAAAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
121 CCCCAGCT 180
121 CCCCAGCT 180
121 CCCCAGCT 180
181 GCCGTTTGGCCACCCCAATCAGACCCAGAGTACATGCTCTCTCTCTCTCTCTCTCT 240
181 GCCGTTTGGCCACCCCAATCAGACCCAGAGTACATGCTCTCTCTCTCTCTCTCTCT 240
181 GCCGTTTGGCCACCCCAATCAGACCCAGAGTACATGCTCTCTCTCTCTCTCTCTCT 240
241 GTCCGATGCTTACAG 300
241 GTCCGATGCTTACAG 300
241 GTCCGATGCTTACAG 300
301 CACCATCAGCAGCTTATTTGACAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
301 CACCATCAGCAGCTTATTTGACAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
361 GAGGTAGCTTTTACATTTAGTGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
361 GAGGTAGCTTTTACATTTAGTGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
421 GATCTTGGGAG 480
421 GATCTTGGGAG 480
421 GATCTTGGGAG 480
481 TGCCAGCTGAG 540
481 TGCCAGCTGAG 540
541 GCGCTCGTGGCAG 600
541 GCGCTCGTGGCAG 600
601 CCGAAACTTTAAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
601 CCGAAACTTTAAGAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
661 GAGCGTGGAG 720
661 GAGCGTGGAG 720

QY 721 CCTGTCTCTGTGTTTGGCCGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 CCTGTCTCTGTGTTTGGCCGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 CCGCTCTGAG 840
DB 781 CCGCTCTGAG 840
QY 841 GCGGCGCCACAG 900
DB 841 GCGGCGCCACAG 900
QY 901 CAGTGGAG 960
DB 901 CAGTGGAG 960
QY 961 ACCCTTGTAG 1020
DB 961 ACCCTTGTAG 1020
QY 1021 CCGGAG 1080
DB 1021 CCGGAG 1080
QY 1081 CACACCCACAG 1140
DB 1081 CACACCCACAG 1140
QY 1141 CTCTGCCAACAAG 1200
DB 1141 CTCTGCCAACAAG 1200
QY 1201 CAGGTAG 1207
DB 1201 CAGGTAG 1207

RESULT 11

AD18317
ID AD18317 standard; DNA; 1207 BP.

AC AD18317;
XX 18-DEC-2001 (first entry)
DE Human MP-52 DNA.

XX Human; MP-52; vulnary; antiinflammatory; analgesic; ligament defect;
KW transforming growth factor-beta; TGF-beta; tissue formation; tendonitis;
KW wound healing; tissue repair; carpal tunnel syndrome; gene therapy; ds.
OS Homo sapiens.

XX Key Location/Qualifiers
FH 845..1207
FT /tag= a
FT /product= "Human MP-52 protein"
FT /note= "CDS does not include start codon"
FT /partial

US6284872-B1.

04-SEP-2001.

28-FEB-1997; 97US-0808324.

22-DEC-1994; 94US-0362670.

07-DEC-1993; 93US-0164103.

25-MAR-1994; 94US-0217780.

02-NOV-1994; 94US-0333576.

(GENY) GENETICS INST INC.
(HAND) HARVARD COLLEGE.

XX	CElestre AJ, Wozniy JM, Rosen VA, Wolman NM, Thomsen GH;
PI	Melton DA;
XX	
DR	WPI: 2001-588978/66.
XX	P-PSDB; AAEL0973.
XX	
PT	New chimeric DNAs, useful for treating tendonitis, carpal tunnel
PM	syndrome and other tendon and ligament defects, comprises DNA encoding
PM	protein linked to DNA encoding bone morphogenetic proteins (BMP)-12,
XX	BMP-13 or Mps2 -
PS	
XX	Disclosure; Column 37-38; 42pp; English.
CC	
CC	The invention relates to a chimeric DNA comprising a DNA sequence
CC	encoding a propeptide from a member of the transforming growth factor
CC	(TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence
CC	encoding an amino acid sequence encoding a mature polypeptide consisting
CC	of Bone Morphogenetic Protein (BMP)-12, BMP-13 or Mps2 protein. The DNA
CC	sequences are useful for producing proteins which induce tendon/ligament
CC	like tissue formation, and for isolating and cloning further DNA
CC	sequences encoding BMP-12 related proteins with similar activity. The
CC	proteins are useful for the induction of tendon/ligament-like tissue
CC	formation, wound healing, ligament and other tissue repair, augmenting
CC	the activity of bone morphogenetic proteins, and for treating tendonitis,
CC	carpal tunnel syndrome and other tendon and ligament defects. The
CC	present sequence is a DNA encoding human MP-12 protein.
XX	
SQ	Sequence 1207 BP; 254 A; 384 C; 370 G; 199 T; 0 other;
Query Match	99.9%; Score 1205.4; DB 22; Length 1207;
Best Local Similarity	99.9%; Pred. No. 7e-249;
Matches 1206; Conservative	0; Mismatches 1; Indels 0; Gaps 0
QY	1 ACCGGGCGGCGCTGTAACCCAGCCAGCAGCACCCTCCCAACAAAGGAGGCTACACCGG 60
DB	1 ACCGGGCGGCGCTGTAACCCAGCCAGCAGCACCCTCCCAACAAAGGAGGCTACACCGG 60
QY	61 GACTGTGACCCCAAAAGAGAGAGCTTCGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB	61 GACTGTGACCCCAAAAGAGAGAGCTTCGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY	121 CCCGAGCT 180
DB	121 CCCGAGCT 180
QY	181 GCGGTTTGCGCCACCCGCCCATACACCCACAGTACATGCTCTGCTGTACAGAGCGT 240
DB	181 GCGGTTTGCGCCACCCGCCCATACACCCACAGTACATGCTCTGCTGTACAGAGCGT 240
QY	241 GTCCGAGCTGTGACAGAAAGGAGGAGCAACAGCAGCGTGAAGTTGAGAGCTTGCCGCCAA 300
DB	241 GTCCGAGCTGTGACAGAAAGGAGGAGCAACAGCAGCGTGAAGTTGAGAGCTTGCCGCCAA 300
QY	301 CACCATCACACACCTTATTTGACAAAGGAGAGGACCGAGGAGGAGGAGGAGGAGGAGGAG 360
DB	301 CACCATCACACACCTTATTTGACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY	361 GAGGTACGTTGACATTAGTCCCTGTGAGAGAGATGGGCTGTGGGGCGAGAGCTCG 420
DB	361 GAGGTACGTTGACATTAGTCCCTGTGAGAGAGATGGGCTGTGGGGCGAGAGCTCG 420
QY	421 GATCTTGGGAG 480
DB	421 GATCTTGGGAG 480
QY	481 TGCCGAGCTGTGACAGCTGTGACAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB	481 TGCCGAGCTGTGACAGCTGTGACAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY	541 GCGGCTTCGTTGCGAGGCTGTGACAGGATGCTGCTGGAGAGTGTTCGATCTGGAAGCTTT 600
DB	541 GCGGCTTCGTTGCGAGGCTGTGACAGGATGCTGCTGGAGAGTGTTCGATCTGGAAGCTTT 600

Chr	Start (kb)	End (kb)	Gene	Transcript	Accession	Length (bp)	GC (%)	GC3 (%)	GC4 (%)	GC5 (%)	GC6 (%)	GC7 (%)	GC8 (%)	GC9 (%)	GC10 (%)	GC11 (%)	GC12 (%)	GC13 (%)	GC14 (%)	GC15 (%)	GC16 (%)	GC17 (%)	GC18 (%)	GC19 (%)	GC20 (%)	GC21 (%)	GC22 (%)	GC23 (%)	GC24 (%)	GC25 (%)	GC26 (%)	GC27 (%)	GC28 (%)	GC29 (%)	GC30 (%)	GC31 (%)	GC32 (%)	GC33 (%)	GC34 (%)	GC35 (%)	GC36 (%)	GC37 (%)	GC38 (%)	GC39 (%)	GC40 (%)	GC41 (%)	GC42 (%)	GC43 (%)	GC44 (%)	GC45 (%)	GC46 (%)	GC47 (%)	GC48 (%)	GC49 (%)	GC50 (%)	GC51 (%)	GC52 (%)	GC53 (%)	GC54 (%)	GC55 (%)	GC56 (%)	GC57 (%)	GC58 (%)	GC59 (%)	GC60 (%)	GC61 (%)	GC62 (%)	GC63 (%)	GC64 (%)	GC65 (%)	GC66 (%)	GC67 (%)	GC68 (%)	GC69 (%)	GC70 (%)	GC71 (%)	GC72 (%)	GC73 (%)	GC74 (%)	GC75 (%)	GC76 (%)	GC77 (%)	GC78 (%)	GC79 (%)	GC80 (%)	GC81 (%)	GC82 (%)	GC83 (%)	GC84 (%)	GC85 (%)	GC86 (%)	GC87 (%)	GC88 (%)	GC89 (%)	GC90 (%)	GC91 (%)	GC92 (%)	GC93 (%)	GC94 (%)	GC95 (%)	GC96 (%)	GC97 (%)	GC98 (%)	GC99 (%)	GC100 (%)	GC101 (%)	GC102 (%)	GC103 (%)	GC104 (%)	GC105 (%)	GC106 (%)	GC107 (%)	GC108 (%)	GC109 (%)	GC110 (%)	GC111 (%)	GC112 (%)	GC113 (%)	GC114 (%)	GC115 (%)	GC116 (%)	GC117 (%)	GC118 (%)	GC119 (%)	GC120 (%)	GC121 (%)	GC122 (%)	GC123 (%)	GC124 (%)	GC125 (%)	GC126 (%)	GC127 (%)	GC128 (%)	GC129 (%)	GC130 (%)	GC131 (%)	GC132 (%)	GC133 (%)	GC134 (%)	GC135 (%)	GC136 (%)	GC137 (%)	GC138 (%)	GC139 (%)	GC140 (%)	GC141 (%)	GC142 (%)	GC143 (%)	GC144 (%)	GC145 (%)	GC146 (%)	GC147 (%)	GC148 (%)	GC149 (%)	GC150 (%)	GC151 (%)	GC152 (%)	GC153 (%)	GC154 (%)	GC155 (%)	GC156 (%)	GC157 (%)	GC158 (%)	GC159 (%)	GC160 (%)	GC161 (%)	GC162 (%)	GC163 (%)	GC164 (%)	GC165 (%)	GC166 (%)	GC167 (%)	GC168 (%)	GC169 (%)	GC170 (%)	GC171 (%)	GC172 (%)	GC173 (%)	GC174 (%)	GC175 (%)	GC176 (%)	GC177 (%)	GC178 (%)	GC179 (%)	GC180 (%)	GC181 (%)	GC182 (%)	GC183 (%)	GC184 (%)	GC185 (%)	GC186 (%)	GC187 (%)	GC188 (%)	GC189 (%)	GC190 (%)	GC191 (%)	GC192 (%)	GC193 (%)	GC194 (%)	GC195 (%)	GC196 (%)	GC197 (%)	GC198 (%)	GC199 (%)	GC200 (%)	GC201 (%)	GC202 (%)	GC203 (%)	GC204 (%)	GC205 (%)	GC206 (%)	GC207 (%)	GC208 (%)	GC209 (%)	GC210 (%)	GC211 (%)	GC212 (%)	GC213 (%)	GC214 (%)	GC215 (%)	GC216 (%)	GC217 (%)	GC218 (%)	GC219 (%)	GC220 (%)	GC221 (%)	GC222 (%)	GC223 (%)	GC224 (%)	GC225 (%)	GC226 (%)	GC227 (%)	GC228 (%)	GC229 (%)	GC230 (%)	GC231 (%)	GC232 (%)	GC233 (%)	GC234 (%)	GC235 (%)	GC236 (%)	GC237 (%)	GC238 (%)	GC239 (%)	GC240 (%)	GC241 (%)	GC242 (%)	GC243 (%)	GC244 (%)	GC245 (%)	GC246 (%)	GC247 (%)	GC248 (%)	GC249 (%)	GC250 (%)	GC251 (%)	GC252 (%)	GC253 (%)	GC254 (%)	GC255 (%)	GC256 (%)	GC257 (%)	GC258 (%)	GC259 (%)	GC260 (%)	GC261 (%)	GC262 (%)	GC263 (%)	GC264 (%)	GC265 (%)	GC266 (%)	GC267 (%)	GC268 (%)	GC269 (%)	GC270 (%)	GC271 (%)	GC272 (%)	GC273 (%)	GC274 (%)	GC275 (%)	GC276 (%)	GC277 (%)	GC278 (%)	GC279 (%)	GC280 (%)	GC281 (%)	GC282 (%)	GC283 (%)	GC284 (%)	GC285 (%)	GC286 (%)	GC287 (%)	GC288 (%)	GC289 (%)	GC290 (%)	GC291 (%)	GC292 (%)	GC293 (%)	GC294 (%)	GC295 (%)	GC296 (%)	GC297 (%)	GC298 (%)	GC299 (%)	GC300 (%)	GC301 (%)	GC302 (%)	GC303 (%)	GC304 (%)	GC305 (%)	GC306 (%)	GC307 (%)	GC308 (%)	GC309 (%)	GC310 (%)	GC311 (%)	GC312 (%)	GC313 (%)	GC314 (%)	GC315 (%)	GC316 (%)	GC317 (%)	GC318 (%)	GC319 (%)	GC320 (%)	GC321 (%)	GC322 (%)	GC323 (%)	GC324 (%)	GC325 (%)	GC326 (%)	GC327 (%)	GC328 (%)	GC329 (%)	GC330 (%)	GC331 (%)	GC332 (%)	GC333 (%)	GC334 (%)	GC335 (%)	GC336 (%)	GC337 (%)	GC338 (%)	GC339 (%)	GC340 (%)	GC341 (%)	GC342 (%)	GC343 (%)	GC344 (%)	GC345 (%)	GC346 (%)	GC347 (%)	GC348 (%)	GC349 (%)	GC350 (%)	GC351 (%)	GC352 (%)	GC353 (%)	GC354 (%)	GC355 (%)	GC356 (%)	GC357 (%)	GC358 (%)	GC359 (%)	GC360 (%)	GC361 (%)	GC362 (%)	GC363 (%)	GC364 (%)	GC365 (%)	GC366 (%)	GC367 (%)	GC368 (%)	GC369 (%)	GC370 (%)	GC371 (%)	GC372 (%)	GC373 (%)	GC374 (%)	GC375 (%)	GC376 (%)	GC377 (%)	GC378 (%)	GC379 (%)	GC380 (%)	GC381 (%)	GC382 (%)	GC383 (%)	GC384 (%)	GC385 (%)	GC386 (%)	GC387 (%)	GC388 (%)	GC389 (%)	GC390 (%)	GC391 (%)	GC392 (%)	GC393 (%)	GC394 (%)	GC395 (%)	GC396 (%)	GC397 (%)	GC398 (%)	GC399 (%)	GC400 (%)	GC401 (%)	GC402 (%)	GC403 (%)	GC404 (%)	GC405 (%)	GC406 (%)	GC407 (%)	GC408 (%)	GC409 (%)	GC410 (%)	GC411 (%)	GC412 (%)	GC413 (%)	GC414 (%)	GC415 (%)
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OY 721 CCTGTTCTGGTGTGTTGGCCGACCAAGAAACGGGACCTGTTCTTTAATGAGATTAAAGC 780
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OY 841 GCGGGCCCCACTGCGCCACTCGCCAGAGGCAAGCCAGACCAAGAACTTAAAGCTCGCTG 900
DB 1404 GCGGGCCCCACTGCGCCACTCGCCAGAGGCAAGCCAGACCAAGAACTTAAAGCTCGCTG 1463
OY 901 CAGTCGAAGGACATGCACTGTCACCTCAAGGACATGGGCTGGAGCACTGGATCATCGC 960
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DB 1524 ACCCTTGAGTACGAGGCTTTCACACTGGAGGGGCTGTCGAGTCCCATTTGCGCTCCCA 1583
OY 1021 CCTGGAGCCCAAGATCATGACATGACACCTGATGAATGACATGACCCGAGTC 1080
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DB 1644 CACACCAACCACTGCTGTGTGCCACGCGGCTGAGTCCCATCAGCATCCTCTTCATTGA 1703
OY 1141 CTCTGCCAACAACGCGTGTATTAAGCAATATGAGACATGTCGTGAGTCGTGTGGCTG 1200
DB 1704 CTCTGCCAACAACGCGTGTATTAAGCAATATGAGACATGTCGTGAGTCGTGTGGCTG 1763
OY 1201 CAGGTAG 1207
DB 1764 CAGGTAG 1770
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Search completed: August 28, 2003, 04:39:53
Job time : 397 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 04:04:14 ; Search time 2886 Seconds

(without alignments)
10164.762 Million cell updates/sec

Title: US-09-901-556C-1

Perfect score: 1207

Sequence: 1 accggcgccctgaacca.....agtcgtgtgctgcagtag 1207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*

1: em_estbda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estl:*
9: gb_estl:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pln:*
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21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	780.8	64.7	819	10	BG750046 602708816
2	779.8	64.6	889	13	BUI68206 AGENCOURT
3	715.8	59.3	1025	10	BF688622 602185258
4	669	55.4	946	13	B0556542 AGENCOURT

5	664.2	55.0	809	10	BG753359	BG753359 602731787
6	651.6	54.0	922	13	B0641867	B0641867 AGENCOURT
7	648.4	53.7	848	12	B0505085	B0505085 603633689
8	647.6	53.7	1242	11	AK041168	AK041168 Mus muscu
9	647.2	53.6	694	10	BG750811	BG750811 602707325
10	628.4	52.1	897	13	B0173828	B0173828 AGENCOURT
11	608.6	50.4	907	13	B0859313	B0859313 AGENCOURT
12	586.6	48.6	712	10	BB637633	BB637633 AGENCOURT
13	559.8	46.4	581	12	B1084366	B1084366 602869884
14	549.4	45.5	918	13	B0854722	B0854722 AGENCOURT
15	516.6	42.8	571	10	BG733101	BG733101 346810 MA
16	511.2	42.4	938	13	B0553725	B0553725 AGENCOURT
17	505.4	41.9	508	13	BX283226	BX283226 AGENCOURT
18	403.8	33.5	479	13	B0563481	B0563481 9103h02.Y
19	398	33.0	846	13	B0856415	B0856415 AGENCOURT
20	397.8	33.0	441	10	BG385196	BG385196 306833 MA
21	338	28.0	617	9	AA790776	AA790776 wv19a07.r
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23	245.2	20.3	661	13	B0169372	B0169372 STR00320
24	235.4	19.5	936	13	B0541856	B0541856 AGENCOURT
25	230.8	19.1	953	10	BF688219	BF688219 602184760
26	221.6	18.4	491	14	CB356254	CB356254 ZEP01-P00
27	214.4	17.8	475	9	AT761284	AT761284 wh9b04.x
28	212.8	17.6	798	13	B0604531	B0604531 MI-P-CP1-
29	211.2	17.5	505	12	B1401488	B1401488 MI-P-CP0-
30	204	16.9	791	13	B0625224	B0625224 UI-H-FG1-
31	200	16.6	563	10	BF044119	BF044119 BP250023A
32	198.2	16.4	543	12	BT559439	BT559439 603252937
33	193	16.0	714	10	BF689009	BF689009 602185258
34	192.6	16.0	552	9	AT641304	AT641304 fc13c07.y
35	181.4	15.0	608	29	CNS015XT	AL165844 Tetradon
36	175.8	14.6	797	10	BG753200	BG753200 602732285
37	172	14.3	683	12	B1084690	B1084690 602869884
38	160.2	13.3	764	10	BG753736	BG753736 602732939
39	158.4	13.1	973	14	CD513413	CD513413 AGENCOURT
40	149.8	12.4	1128	13	B0854723	B0854723 AGENCOURT
41	147.8	12.2	718	12	BG870679	BG870679 602791665
42	139.4	11.5	718	12	BM684858	BM684858 UI-E-EJ1-
43	139	11.5	685	12	BM931289	BM931289 UI-E-EJ1-
44	139	11.5	793	10	BG187538	BG187538 RST6663 A
45	139	11.5	928	13	B0535475	B0535475 AGENCOURT

ALIGNMENTS

RESULT 1
LOCUS 819 bp mRNA linear EST 15-MAY-2001
DEFINITION 602708816P1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4845555 5',
mRNA sequence.
ACCESSION BG750046
VERSION BG750046.1 GI:14060699
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 819)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMN at:
<http://image.llnl.gov>
Plate: L10CM1684 row: p column: 04
High quality sequence stop: 812.

FEATURES

location/Qualifiers

1 819
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:484555"
/issue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. I"

BASE COUNT

164 a 244 c 273 g 138 t

ORIGIN

Query Match 64.7% Score 780.8; DB 10; Length 819;
Best Local Similarity 98.4%; Pred. No. 6,1e-162;
Matches 815; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

181 GCGCTTGGCCACCCCATACACCCACAGATACATCTCTCCGTGACAGACGCT 240
|||||
2 GCGCTTGGCCACCCCATACACCCACAGATACATCTCTCCGTGACAGACGCT 61
|||||
241 GTCCGATGCTGACGAAAGGAGGCAACGACGCTGAGAGCTGGCTGGCCAA 300
|||||
62 GTCCGATGCTGACGAAAGGAGGCAACGACGCTGAGAGCTGGCTGGCCAA 121
|||||
301 CACCATCACCAGCTTTATTGCAAAAGGCAAGATGACCGAGTCCCTGGTCAAGACA 360
|||||
122 CACCATCACCAGCTTTATTGCAAAAGGCAAGATGACCGAGTCCCTGGTCAAGACA 181
|||||
361 GAGTAGCTGTTGACATTAAGTCCCTGAGAGAGATGGCTGGGGGCCAGCTGCG 420
|||||
182 GAGTAGCTGTTGACATTAAGTCCCTGAGAGAGATGGCTGGGGGCCAGCTGCG 241
|||||
421 GATTTGCGGAAGAGCCCTCGGACACGCGCCAGCCGCGGAGGCGGGGCG 480
|||||
242 GATTTGCGGAAGAGCCCTCGGACACGCGCCAGCCGCGGAGGCGGGGCG 301
|||||
481 TGCCGACCTGAAGCTGTCAGACTGCCCCACGCGCGCGCTCTCTGCTGATGT 540
|||||
302 TGCCGACCTGAAGCTGTCAGACTGCCCCACGCGCGCGCTCTCTGCTGATGT 361
|||||
541 GCGCTCCGTCGACGCGCTGAGAGGATGCTGGAGGTTGACATCTGAAGCTCTT 600
|||||
362 GCGCTCCGTCGACGCGCTGAGAGGATGCTGGAGGTTGACATCTGAAGCTCTT 421
|||||
601 CCGAACTTTAAGAACTCGGCCCAAGCTGCTCTGAGCTGAGAGCTGGGAAAGCGAG 660
|||||
422 CCGAACTTTAAGAACTCGGCCCAAGCTGCTCTGAGCTGAGAGCTGGGAAAGCGAG 481
|||||
661 GCGCTGAGACCTCGCTGGCTGAGCTGAGCGGCGCGCGGAGGCTCCAGAGAGCG 720
|||||
482 GCGCTGAGACCTCGCTGGCTGAGCTGAGCGGCGCGGAGGCTCCAGAGAGCG 541
|||||
721 CCGTTCCTGCTGTTGGCGGACCAAGAAAGGAGGAGCTTCTTTAAGAGTTAAAGC 780
|||||
542 CCGTTCCTGCTGTTGGCGGACCAAGAAAGGAGGAGCTTCTTTAAGAGTTAAAGC 601
|||||
781 CCGCTGCGGACGACATTAAGACCGTGTATGATACCTTTACAGCAGGCGGAAACG 840
|||||
602 CCGCTGCGGACGACATTAAGACCGTGTATGATACCTTTACAGCAGGCGGAAACG 661
|||||
841 GCGGGCCCACTGCGCACTGCGCAAGGCGCAAGCAGCAGCAGCAGCAGCAGCAGCAG 900
|||||
662 GCGGG-CCCACTGCGCACTGCGCAAGGCGCAAGCAGCAGCAGCAGCAGCAGCAGCAG 720
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901 CAGTCGGAAGGCACTGATGTCAACCTTCAAGGACATGGGCT-GGAGGACTGATCATG 959
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FEATURES

location/Qualifiers

1 889
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6074625"
/issue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT

179 a 276 c 279 g 155 t

ORIGIN

Query Match 64.6% Score 779.8; DB 13; Length 889;
Best Local Similarity 98.3%; Pred. No. 1e-161;
Matches 799; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

295 GCGCAACACATCACCTTTATTGACAAAGGCAAGATGACGAGTCCCTGCTGAC 354
|||||
1 GCGCAACACATCACCTTTATTGACAAAGGCAAGATGACGAGTCCCTGCTGAC 60
|||||
355 GAAGCAGAGTACGTTGACATTAGTGCCTTGAGAGAGATGGCTGCTGGGGCGCA 414
|||||
61 GAAGCAGAGTACGTTGACATTAGTGCCTTGAGAGAGATGGCTGCTGGGGCGCA 120
|||||
415 GCTGCGGATCTTGGGGAAGAGCCCTGCGACACGCGCAAGCAGCGGCCCGAGGCGG 474
|||||
121 GCTGCGGATCTTGGGGAAGAGCCCTGCGACACGCGCAAGCAGCGGCCCGAGGCGG 180
|||||
475 GCGGCTGCGCAGCTGAAGCTGTGACGCTGCGGAGGCGCGGAGCGCGCTTGGCT 554
|||||

[illegible]

Query Match	Best Local Match	Similarity	Score	DB	Length
Query 736; Conservative	59.3%; 98.0%;	715.8;	10;	1025;	
	Pred. No. 1.4e-147;				
	Mismatches 12; Indels 3; Gaps 1				
460	GGCCCCCGGAGAGCGGGCGGGCTGCCACACTGACGTGTCACAGTCCCGCAGCGCGCGCA	519			
Db	2	GGCCCCCGGAGAGCGGGCGGGCTGCCACACTGACGTGTCACAGTCCCGCAGCGCGCGCA	61		
Qy	520	GCCGCGCTCTTGGTGTGATGTGCGCTCGCTGACAGCGCTGACAGGATCTGGCTGGAGGT	579		
Db	62	GCCGCGCGCTCTTGGTGTGATGTGCGCTCGCTGACAGCGCTGACAGGATCTGGCTGGAGGT	121		
Qy	580	GTTCGACATCTGGAGAGCTCTTCCGAACTTTAAGACATCGGCGCCAGCTGTGCTGGAGCT	639		
Db	122	GTTCGACATCTGGAGAGCTCTTCCGAACTTTAAGACATCGGCGCCAGCTGTGCTGGAGCT	181		
Qy	640	GGAGGCGCTGGGAAAGGGGCGAGGGCGGTGACCTCGGTGGCGTGGGCTTCGACCGGGCGC	699		
Db	182	GGAGGCGCTGGGAAAGGGGCGAGGGCGGTGACCTCGGTGGCGTGGGCTTCGACCGGGCGC	241		
Qy	700	CCGCGAGGTCACAGAGAAAGCCCTGTGCTGGTGTGTTGGCCGACACCAAGAAAGGGAGCT	759		
Db	242	CCGCGAGGTCACAGAGAAAGCCCTGTGCTGGTGTGTTGGCCGACACCAAGAAAGGGAGCT	301		
Qy	760	GTTCCTTAATAGATTAAGGGCCCGCTCGGCGACAGCATTAAGACCGTGTATGACTACT	819		
Db	302	GTTCCTTAATAGATTAAGGGCCCGCTCGGCGACAGCATTAAGACCGTGTATGACTACT	361		
Qy	820	GTTCAGCCAGAGGGGAGAAAGCGGGGGCCCACTGTGSCACTGTGCGCAGGCGAAGCGACAG	879		
Db	362	GTTCAGCCAGAGGGGAGAAAGCGGGGGCCCACTGTGSCACTGTGCGCAGGCGAAGCGACAG	421		
Qy	880	CAAGAACCTTAAAGGCTCGCTGACGTGCGAAGGCACTGCATGTCAACTTCAAGAGACATGGG	939		
Db	422	CAAGAACCTTAAAGGCTCGCTGACGTGCGAAGGCACTGCATGTCAACTTCAAGAGACATGGG	481		
Qy	940	CTGGGAGACATGAGATCATCGACACCCCTTGGAGTACAGAGCTTTCCACTGTGAGGGGCTGTG	999		
Db	482	CTGGGAGACATGAGATCATCGACACCCCTTGGAGTACAGAGCTTTCCACTGTGAGGGGCTGTG	541		
Qy	1000	CGAGTTCGATTTGGCGTCCCACTGTGAGAGCCCAAGCATATCATGCAAGTCAACAGCCCTGAT	1055		
Db	542	CGAGTTCGATTTGGCGTCCCACTGTGAGAGCCCAAGCATATCATGCAAGTCAACAGCCCTGAT	601		
Qy	1060	GAATCCATGAGACCCCGAGTCCACACACCAACCAACGTCGTGTGCCAGAGCGGCTGATGCC	1113		
Db	602	GAATCCATGAGACCCCGAGTCCACACACCAACCAACGTCGTGTGCCAGAGCGGCTGATGCC	661		
Qy	1120	CATCAGCATCTCTTTCATTTGACTGTGCAACAGAGTGTGTATTAAGCATGTATGAGAGAT	1175		
Db	662	CATCAGCATCTCTTTCATTTGACTGTGCAACAGAGTGTGTATTAAGCATGTATGAGAGAT	721		
Qy	1180	GGTC---GTGAGTGTGTGTGGCTGCAGGTAG 1207			
Db	722	TGGCTGTGTGAGCGCGTGTGGGTGCAGGTAG 752			

RESULT 4
 BUS56542/c 946 bp mRNA linear EST 16-SEP-2002
 LOCUS AGENCOURT.1018518 NIH_MGC.109 Homo sapiens cDNA clone
 DEFINITION IMAGE:5584250 5', mRNA sequence.
 ACCESSION BUS56542
 VERSION BUS56542.1 GI:22906814
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://mgi.nhl.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2794 row: e column: 18
 High quality sequence stop: 676.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_109"
 /note="Organ: Ovary; Vector: pOTB7; Site:1: EcoRI; Site:2:
 XhoI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

BASE COUNT 195 a 275 c 295 g 181 t
 ORIGIN

Query Match 55.4%; Score 669; DB 13; Length 946;
 Best Local Similarity 95.4%; Pred. No. 3e-137;
 Matches 711; Conservative 0; Mismatches 30; Indels 4; Gaps 2;

QY 467 GGAGCGGGGGGGCTGCCAGCTGAAGCTGTCACAGTCCCGGCGG--CACCG 523
 DB 940 GCGGGGGGGGGCTGCCAGCTGAAGAGGGTCCAGCTGCCCAAGGGGCGGCCAGCGG 881
 QY 524 GCTCTCTGATGATGTCGCTCCGTCGACAGGCTGACGATCTGCTGGAGCTTC 583
 DB 880 GCCCGCTGCTGGAATGCGCTCGTGCAGGCTGACGATCTGCTGGAGCTTC 821
 QY 584 GACATCTGAGAGCTCTCCGAACTTAAAGACTGCGCCAGCTGCTGAGAGCTGAG 643
 DB 820 GACATCTGAGAGCTCTCCGAACTTAAAGACTGCGCCAGCTGCTGAGAGCTGAG 761
 QY 644 GCTCTGGAAGGGGGA--GGCGCTGAGAGCTCCGTCGCTGAGCGCGCGCGCG 702
 DB 760 GCTCTGGAAGGGGGA--GGCGCTGAGAGCTCCGTCGCTGAGCGCGCGCGCG 701
 QY 703 GCAGCTCCAGAGAGGGGCTCTCTGCTGTTGGCCGACCAAGAAAGGAGCTGTT 762
 DB 700 GAGGCTCCAGAGAGGGGCTCTCTGCTGTTGGCCGACCAAGAAAGGAGCTGTT 641
 QY 763 CTTTAATGATTAAGGGCGCTCTGCGCAGAGAGATTAAGACCGTGTATGATGCTGTT 822

Db 640 CTTTAATGATTAAGGGCGCTCTGCGCAGAGAGATTAAGACCGTGTATGATGCTGTT 581
 QY 823 CAGCGAGGGGCGGAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 882
 Db 580 CAGCGAGGGGCGGAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 521
 QY 883 GAACCTTAAGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942
 Db 520 GAACCTTAAGGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 461
 QY 943 GAGAGCTGATCATGACACCCCTTGAATGAGAGGCTTCCAGTCCGAGGGGGCTGTCGA 1002
 Db 460 GAGAGCTGATCATGACACCCCTTGAATGAGAGGCTTCCAGTCCGAGGGGGCTGTCGA 401
 QY 1003 GTTCCCATGCGCTCCGACCTGAGAGCCCGACGAAATCATGATCATGACACCTGATGAA 1062
 Db 400 GTTCCCATGCGCTCCGACCTGAGAGCCCGACGAAATCATGATCATGACACCTGATGAA 341
 QY 1063 CTCATGAGACCCGAGTCCACACACACACACACACACACACACACACACACACACAC 1122
 Db 340 CTCATGAGACCCGAGTCCACACACACACACACACACACACACACACACACACACAC 281
 QY 1123 CAGCATCCCTTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
 Db 280 CAGCATCCCTTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 221
 QY 1183 CGTGAGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1207
 Db 220 CGTGGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 196

RESULT 5
 BG753359 809 bp mRNA linear EST 15-MAY-2001
 LOCUS BG753359
 DEFINITION 602731787F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4875453 5',
 mRNA sequence.
 ACCESSION BG753359
 VERSION BG753359.1 GI:14064012
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://mgi.nhl.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM1756 row: m column: 22
 High quality sequence stop: 773.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image:4875453
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_43"
 /note="Organ: eye; Vector: pOTB7; Site:1: XhoI; Site:2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC library. 1"

BASE COUNT 160 a 243 c 264 g 142 t

ORIGIN

Query Match 55.0%; Score 664.2; DB 10; Length 809;

Best Local Similarity 96.2%; Pred. No. 3.2e-136;

Matches 755; Conservative 0; Mismatches 23; Indels 7; Gaps 7;

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OY 310 CAGCTTTATTTGACAAAGGCGCAAGATGACCGAGGTCCTCGTTCAGAGAGCAGAGTACT 369
DB 2 CAGCTTTATTTGACAAAGGCGCAAGATGACCGAGGTCCTCGTTCAGAGAGCAGAGTACT 61
OY 370 GTTTCACATTTAGTGGCCCTGAGAGAGATGGCTGCTGGGGCCGAGCTGCGGATTCG 429
DB 62 GTTTCACATTTAGTGGCCCTGAGAGAGATGGCTGCTGGGGCCGAGCTGCGGATTCG 121
OY 430 GAAGAAAGCCCTGAGACAGCGCCAAAGCCAGCGCCCGGAGGCGGGCTGCCACACT 489
DB 122 GAAGAAAGCCCTGAGACAGCGCCAAAGCCAGCGCCCGGAGGCGGGCTGCCACACT 181
OY 490 GAAGCTGTCCAGCTGCCCCAGCGCCGAGCCGCTCTTCTGCTGATGTGCCCTCGT 549
DB 182 GAAGCTGTCCAGCTGCCCCAGCGCCGAGCCGCTCTTCTGCTGATGTGCCCTCGT 241
OY 550 GCCAGGCTGAGCAGATGCTGCTGGAGATGTTTCGACATCTGAAGCTCTTCCGAACTT 609
DB 242 GCCAGGCTGAGCAGATGCTGCTGGAGATGTTTCGACATCTGAAGCTCTTCCGAACTT 301
OY 610 TAAAGACTCGGCCAGCTGTGCTGG-AGCTGAGAGCCCTGGGAACGGGGGAGGCGCTGG 668
DB 302 TAAAGACTCGGCCAGCTGTGCTGG-AGCTGAGAGCCCTGGGAACGGGGGAGGCGCTGG 361
OY 669 ACCGCGGCGCTGGGCTGCTGCAACCGCGCGCCGCGAGCTCCAGAGAGAGCCCTGG-7TC 727
DB 362 ACCGCGGCGCTGGGCTGCTGCAACCGCGCGCCGCGAGCTCCAGAGAGAGCCCTGGCTTC 421
OY 728 CTGCTGTGTTGGCCGACCAAGAAAGGAGCTGTTCTTTAA-TGAGATTAAAGCCCGCTC 786
DB 422 CTGCTGTGTTGGCCGACCAAGAAAGGAGCTGTTCTTTAA-TGAGATTAAAGCCCGCTC 481
OY 787 TGCGCAGAGCATTAAGACCGTGTATGATGATCTGTTACGCCAGCGGCGAAAGCGCGGC 846
DB 482 TGCGCAGAGCATTAAGACCGTGTATGATGATCTGTTACGCCAGCGGCGAAAGCGCGGC 541
OY 847 CCCAGCTGGCCACTGGCCAGGCGAGCGACCCAGAGAAAGCTTAAAGCTGCTGCTGACATCG 906
DB 542 CCCAGCTGGCCACTGGCCAGGCGAGCGACCCAGAGAAAGCTTAAAGCTGCTGCTGACATCG 601
OY 907 GAAGGCACTGCATGTCAACTTCAAGGACATGGCTGGGAGCAG-TGATCATCGACACCC 965
DB 602 GAAGGCACTGCATGTCAACTTCAAGGACATGGCTGGGAGCAG-TGATCATCGACACCC 661
OY 966 -TTGATGACAGAGGCTTTTCACTGCGAGGGGCTGTGCGATTCCATTGCGCTCCACCTG 1024
DB 662 TTTGATGACAGAGGCTTTTCACTGCGAGGGGCTGTGCGATT-CCATTGCGCT-CCAACTG 719
OY 1025 GAGGCCAGATTCATGAGCTGATCCAGACCCCTGATGAACTCCATGAGACCCGAGTCCACA 1084
DB 720 GAGGCCAGATTCATGAGCTGATCCAGACCCCTGATGAACTCCATGAGACCCGAGTCCACA 779
OY 1085 CCACC 1089
DB 780 CCACC 784

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RESULT 6
LOCUS B0641867
DEFINITION AGENCOURT 8287210 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292363
ACCESSION B0641867

VERSION B0641867.1 GI:21766039
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 922)

AUTHORS NIH-MGC <http://imgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

CONTACT: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: ILICM2493 row: k column: 20

High quality sequence stop: 655.

FEATURES

Location/Qualifiers

1..922

/organism="Homo sapiens"

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/lab_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pOTB7; Site:1; XhoI; Site:2; EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAGAG(G) library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. 1"

BASE COUNT 206 a . 311 c 281 g 123 t 1 others

ORIGIN

Query Match 54.0%; Score 651.6; DB 13; Length 922;

Best Local Similarity 96.7%; Pred. No. 2e-133;

Matches 676; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

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OY 1 ACCGGGCGGCGCTTAACCCAGCAGACACCTTCCCAACAGGCGCTACAGCCG 60
DB 39 ACCGGGCGGCGCTTAACCCAGCAGACACCTTCCCAACAGGCGCTACAGCCG 98
OY 61 GACTGTGACCCCAAAAGGAGAGCTTCCGAGGAGCAAGGACACCCCAAAAGCAGATCTGT 120
DB 99 GACTGTGACCCCAAAAGGAGAGAGCTTCCGAGGAGCAAGGACACCCCAAAAGCAGATCTGT 158
OY 121 CCCAGCTCTCTCTCTGTAAGAAAGCCAGGAGCGCGGCGCCACAGAGAGCCCAAGGA 180
DB 159 CCCAGCTCTCTCTCTGTAAGAAAGCCAGGAGCGCGGCGCCACAGAGAGCCCAAGGA 218
OY 181 GCGGTTTGCGCCACCCCATCACACCCAGAGAGTGTCTGCTGCTGACAGAGCT 240
DB 219 GCGGTTTGCGCCACCCCATCACACCCAGAGAGTGTCTGCTGCTGACAGAGCT 278
OY 241 GTCCGATGCTGACAAAGGAGGAGCAACAGCAGCTGAATTTGAGAGCTGCTGCGCA 300
DB 279 GTCCGATGCTGACAAAGGAGGAGCAACAGCAGCTGAATTTGAGAGCTGCTGCGCA 338
OY 301 CACCATCACAGCTTTATTTGACAAAGGCAAGATGACCGAGTCCCGTGTACAGAAACA 360
DB 339 CACCATCACAGCTTTATTTGACAAAGGCAAGATGACCGAGTCCCGTGTACAGAAACA 398
OY 361 GAGGTAGCTGTTTACATTTAGTGGCCCTGAGAAAGATGAGGTGCTGGGGCGGAGCTGGC 420
DB 399 GAGGTAGCTGTTTACATTTAGTGGCCCTGAGAAAGATGAGGTGCTGGGGCGGAGCTGGC 458

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QY 421 GATCTGGGAAAGCCCTCGGACAGGCGCCAGCCAGCGGCCCGGAGCGCGGC 480
 Db 459 GATCTGGGAAAGCCCTCGGACAGGCGCCAGCCAGCGGCCCGGAGCGCGGC 518
 QY 481 TGCCAGCTGAAGCTGTCCAGTCCCGAGCGCGCCAGCCAGCGGCCCTCTTGATGT 540
 Db 519 TGCCAGCTGAAGCTGTCCAGTCCCGAGCGCGCCAGCCAGCGGCCCTCTTGATGT 578
 QY 541 GCGCTCGTCCAGGCTGAGAGATCTGGCTGGAGAGTGTTCGATCTGGAAGCTTT 600
 Db 579 GCGCTCGTCCAGGCTGAGAGATCTGGCTGGAGAGTGTTCGATCTGGAAGCTTT 638
 QY 601 CGGAACCTTAGAAGCTGGCCGAGCTGTGCTGGAGAGTGTTCGATCTGGAAGCTTT 657
 Db 639 CGGAACCTTAGAAGCTGGCCGAGCTGTGCTGGAGAGTGTTCGATCTGGAAGCTTT 698
 QY 658 CAGGCGCGTGGACCTTCCTGGCTGGCTGGCTGGACCGGC 696
 Db 699 GGGGCGGTGGACCTTCCTGGCTGGCTGGCTGGACCGGC 737

RESULT 7 848 bp mRNA linear EST 07-NOV-2001
 LOCUS BM050865 603633689F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:5423926 5',
 DEFINITION mRNA sequence.

ACCESSION BM050865
 VERSION BM050865.1 GI:16780132
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 848)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaabs-remail.nih.gov

FEATURES
 source
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BASE COUNT 170 a 249 c 271 g 158 t
 ORIGIN

Query Match 53.7%; Score 648.4; DB 12; Length 848;
 Best Local Similarity 96.0%; Pred. No. 1e-132;
 Matches 741; Conservative 0; Mismatches 21; Indels 10; Gaps 7;
 QY 352 CAGGAAGCAGAGGTACGTGTTGACA-TTAGTGCCCTGAGAGATGAGCGCTGGGG 410

Db 2 CAGGAAGCAGAGGTACGTGTTGACA-TTAGTGCCCTGAGAGATGAGCGCTGGGG 61
 QY 411 CCGAGCTGCGGATCTTGGGAAAGAGCCCTTCGACACAGGCGCCAGCGGCCCGGAG 470
 Db 62 CCGAGCTGCGGATCTTGGGAAAGAGCCCTTCGACACAGGCGCCAGCGGCCCGGAG 121
 QY 471 GCGGCGGCGGTGCGGCTGAGAGCTGTCCAGCTGCCCCAGCGCGCGGAGCGCTTCCT 530
 Db 122 GCGGCGGCGGTGCGGCTGAGAGCTGTCCAGCTGCCCCAGCGCGCGGAGCGCTTCCT 181
 QY 531 TGTGTGATGTGGCTGCTCCGCGCA-GGCTGAGAGATCTGTGCTGGAGTGTTCGACATC 589
 Db 182 TGTGTGATGTGGCTGCTCCGCGCA-TGGCTGAGAGATCTGTGCTGGAGTGTTCGACATC 241
 QY 590 TGAAGCTTTCGAAACTTTAAGAACTC--GGCCAGCTGTGCTGAGCTGAGAGCT 647
 Db 242 TGAAGCTTTCGAAACTTTAAGAACTC-TGGCCATGCTGTGCTGAGCTGAGAGCT 301
 QY 648 GGGAGCGGGCAGGGCCGTGACCTCCGTGGCTGGCTGAGAGCTGAGAGCTGAGAGCT 707
 Db 302 GGGAGCGGGCAGGGCCGTGAGCTCCGTGGCTGGCTGAGAGCTGAGAGCTGAGAGCT 361
 QY 708 TCCACGAGAAAGGCGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 767
 Db 362 TCCACGAGAAAGGCGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
 QY 768 ATGAGATTAAAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 827
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 QY 828 AGCGCGGAAAGCG 887
 Db 482 AGCGCGGAAAGCG 541
 QY 888 TTAAGGCTGCGCGAGTGGAGAGGACGATGCAATGCAATCA--GGACATGGGCTGGGA 945
 Db 542 TTAAGGCTGCGCGAGTGGAGAGGACGATGCAATGCAATCAATCAAGGACATGGGCTGGGA 601
 QY 946 CGACTGATCATGCAACCCCTTGGATGACGAGGCTTTCACCTGCGAGGGCTGTGC-GAGT 1004
 Db 602 CGACTGATCATGCAACCCCTTGGATGACGAGGCTTTCACCTGCGAGGGCTGTGCAGT 661
 QY 1005 TCCCATTTGCGCTCCCACTGAGCCAGATCATGCAATGCAATGCAATGCAATGCAAT 1062
 Db 662 TCCCATTTGCGCTCCCACTGAGCCAGATCATGCAATGCAATGCAATGCAATGCAAT 721
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 Db 722 TTCATGAGACCCGAGTCCACACACCAACCACTGTGTGTGCGCCACCGCGCT 773

RESULT 8 1242 bp mRNA linear HTC 05-DEC-2002
 LOCUS AK041168
 DEFINITION Mus musculus adult male aorta and vein cDNA, RIKEN full-length factor 5, full insert sequence.
 ACCESSION AK041168
 VERSION AK041168.1 GI:26334258
 KEYWORDS HTC; CAP trapper
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

OY	938	GGCTGGGAGACAGTGATTCATTCGACCCCTTGGAGTATCGAGGCTTTCACACTGCGAGGGCTG	997
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OY	1058	ATGAACTCCATGSAACCCGAGTCCACACACCACCTGCTGTGGGCCACAGCGGCGAGT	1117
Db	602	ATGAACTCCATGSAACCCGAGTCCACACACCACCTGCTGTGGGCCACAGCGGCGAGT	661
OY	1118	CCGACGAGATCTCTTCATTGACTCTGCCAACAACGTGTGTATTAAGAGATGATGAGC	1177
Db	662	CCGATTAAGATCTCTTCATTGACTCTGCCAACAACGTGTGTATTAAGAGATGATGAGC	721
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Db	722	ATGAGTCGAGATCTGTGGCTGAGGTAG	751

RESULT 9	694 bp	MRNA	linear	EST 15-MAY-2001
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LOCUS	602207325251	NTM_MGC_43	Homo sapiens	clone IMAGE:843686 5',
DEFINITION	mRNA sequence.			
ACCESSION	BG750811			
VERSION	BG750811.1	GI:14061464		
KEYWORDS	EST.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens (human)			
	Homo sapiens			

REFERENCE	Mammalian Gene Collection (MGC)
AUTHORS	1 (bases 1 to 694)
TITLE	NIH-MGC http://mgc.ncl.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished
CONTACT	Robert Struelens

Tissue repository: atml1.nhl.gov
 CDNA library provider: ATCC
 CDNA library arrived by: [imc.mcgill.ca](mailto:image@imc.mcgill.ca)
 DNA sequencing by: Invertebrate Genomics Consortium (ILNLT)
 Clone distribution: MGC clone distribution
 Information can be
 found through the I.M.A.G.E. Consortium/ILNLT at:
<http://image.llnl.gov>
 High quality sequence row: b column: 07
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 Location/Qualifiers
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EcoRI; cDNA made by oligo-OT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GCGACGAG(C). Library constructed by Ling Hong
at the Laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT
ORIGIN
155 a 223 c 219 g 96 t 1 others

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Best Local Similarity	99.58%	Pred. No. 1.7e-132;		
Matches 649;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 1 ACCGGGCGCCCTGAAACCAAGCCAGACACCTCCCAACAAACAGCCAGACTACGCCCG 60

Db	42	ACCGGGGCGGCTTAACCCAAAGCCAGACACCTCCCAACAAAGGAGGCTAAGCCG	10
Qy	61	GACTGTGACCCCAAAAGAGACGTTCCCGAGGCAAGGCACCCCAAAAGAGATCTG	12
Db	102	GACTGTGACCCCAAAAGAGACGTTCCCGAGGCAAGGCACCCCAAAAGAGATCTG	16
Qy	121	CCCGAGTCCCTCTGTGTGAAAGAGCCAGGGAGCCCGGGCCCCACAGAGGCCAAAGA	18
Db	162	CCCGAGTCCCTCTGTGTGAAAGAGCCAGGGAGCCCGGGCCCGCAAGAGGCCAAAGA	22
Qy	181	GCGCTTTCGGCCACCCCCCATCACACCCACAGATACATGCTTCGTGTACAGCAAGCT	24
Db	222	GCGCTTTCGGCCACCCCCCATCACACCCACAGATACATGCTTCGTGTACAGCAAGCT	28
Qy	241	GTCGAGTGCAGAGAAAGGAGGCAACAGCAGCTGAATTTGAGAGCTGGGCTGCCAA	30
Db	282	GTCGAGTGCAGAGAAAGGAGGCAACAGCAGCTGAATTTGAGAGCTGGGCTGCCAA	34
Qy	301	CACCATCACACCTTATTGACAAAGGCCAAGATGACCGAGTCCCGTGTGAGAAACA	36
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Qy	361	GAGGTACGTTTGTGACATTAGTGCCTCGGAGAAAGATGAGGCTGTGGGGGCGAGCTGC	42
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Qy	421	GATCTTGGGGAAGAGCCCTCGGACACGGCCAAAGCCAGCGGCCCCCGGAGGCGGGCGGC	48
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Qy	481	TGCCAGTGAAGTGTGCCAGCTGCCCCACGCGCGGCAAGCCGAGCTCTTGTGAGATG	54
Db	522	TGCCAGTGAAGTGTGCCAGCTGCCCCACGCGCGGCAAGCCGAGCTCTTGTGAGATG	58
Qy	541	GCGCTCGGTCAGAGGCTTGGAGAGATCTGGCTGGAGAGTGTTCGACATCTGGAAGCTCTT	60
Db	582	GCGCTCGGTCAGAGGCTTGGAGAGATCTGGCTGGAGAGTGTTCGACATCTGGAAGCTCTT	64
Qy	601	CCGAAACTTTAAGAACTCGGCCACACTGTGCTGAGCTGGAGGCTCGGAA	62
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RESULT	10
LOCUS	BUI73828
DEFINITION	BUI73828
ACCESSION	AGENDCOURT_7560995 NIH_MGC_112 Homo sapiens mRNA linear EST 04-SEP-2002
VERSION	5' UTR RNA sequence.
KEYWORDS	BUI73828 GI:22687812
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 897)
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapds@mail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) Clone sequencing by: Agencourt Bioscience Corporation DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LINC2290 row: j column: 17 High quality sequence start: 7 High quality sequence stop: 376. Location/Qualifiers
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 BASE COUNT 202 a 294 c 284 g 117 t
 ORIGIN

Query Match 52.1%; Score 628.4; DB 13; Length 897;
 Best Local Similarity 94.2%; Pred. No. 2.7e-128;
 Matches 676; Conservative 0; Mismatches 36; Indels 6; Gaps 2;

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 61 GACTGTGACCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
 152 GACTGTGACCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 211
 121 CCCGAGCTCTCTCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 212 CCCGAGCTCTCTCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 271
 181 GCGGTTTGGCCACCCCATACACCCGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
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 241 GTCGATGCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 332 GTCGATGCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 391
 301 CACCATCACCAGCTTTATGACAAAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 392 CACCATCACCAGCTTTATGACAAAGGAGGAGGAGGAGGAGGAGGAGGAG 451
 361 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 452 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 511
 421 GATCTTGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
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 481 TCCCAAGCTGAAGCTGTCCAGTGCAGCGCGGAGCGCGGCTCTTCTGAGAT 540
 572 TCCCAAGCTGAAGCTGTCCAGTGCAGCGCGGAGCGCGGCTCTTCTGAGAT 631
 541 GCGCTCCGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 632 GCGCTCCGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 691
 601 CCGAAGCTTTAAGAGCTGCGCCAGCTGTGAGGAGGAGGAGGAGGAGGAGG 657
 692 CCGAAGCTTTAAGAGCTGCGCCAGCTGTGAGGAGGAGGAGGAGGAGGAGG 751
 658 -CAGGAGCGGTGAGCTCCGTG--CCTGGGCTTTCAGACGCGCGCGGAGGAGTCCAC 712
 752 AAGGAGCGGTGAGCTCCGTG--CCTGGGCTTTCAGACGCGCGCGGAGGAGTCCAC 809

RESULT 11

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 LOCUS
 DEFINITION
 AGENCOURT 10422919 NIH_MGC_109 Homo sapiens cDNA clone
 IMAGE:6650156 5', mRNA sequence.
 B0859313
 ACCESSION
 VERSION
 B0859313.1 GI:24044305
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 907)
 NIH_MGC http://mhc.nci.nih.gov/
 TITLE
 JOURNAL
 UNPUBLISHED
 CONTACT: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM2894 row: 0 column: 20
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 BASE COUNT 193 a 255 c 284 g 173 t 2 others
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Query Match 50.4%; Score 608.6; DB 13; Length 907;
 Best Local Similarity 97.7%; Pred. No. 6.2e-124;
 Matches 670; Conservative 0; Mismatches 10; Indels 6; Gaps 5;

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 819 GGACATCTGGAAGCTTCTTCCGAAACTTTAAGANCTCGGCCAGCTGTG-TGAGAGCTGG 761
 642 AGGCTGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 701
 760 AGGCTGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 702
 702 GGCAGGTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 761
 701 GGCAGGTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 642
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 822 TCAGCCAGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 881
 581 TCAGCCAGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 522

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[illegible]

ORGANISM	REFERENCE	AUTHORS
Mus musculus (house mouse)		
Eukaryota; Metazoa: Chordata; Vertebrata; Euteleostomi:		
Mammalia: Eumelia: Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
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Arakawa, T.		
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, D., Shida, K., Shinozawa, A., Sakai, C., Nakai, K., Ohno, H., Takeda, Y., Tanaka, T., Toyota, T.,		
Muramatsu, M., Tagawa, A., Takahashi, Y., Takeda, Y., Suzuki, H.,		
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)		
Unpublished		
Controlled		

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
1-7-22 Shinhoh of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome_researc.riken.go.jp,
Carninci.P.genome.gsc.riken.go.jp/
, M., Kono, H., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
Prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujikawa, S., Inoue, K., Togawa, Y.,
Matsui, M., Yoneda, Y., Ishikawa, T., Ozawa, Y., Iizawa, M., Ohara, E.,
Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Kono, H., Fukushima, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001).
K. Yamada, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Ishii, T., Fukushima, S., Harai, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, M., and Hayashizaki, Y.
Mammals of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Funct. Genomics 2 pre, L72-L86 (2001).
Please contact our web site (<http://genome.gsc.riken.go.jp>) for further details.
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Features
Source
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7102
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7102
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/clone_lib="RIKEN full-length enriched, adult male aorta and vein"
/note="Site.1: Sali; Site.2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopaedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare 15 mouse tissues. 1st strand cDNA was primed with a primer 15 mouse tissues. 1st strand cDNA was prepared by using trehalase thermo-activated reverse transcriptase and subsequent enrichment for full-length transcripts. cDNA was prepared through one round of normalization strategy. cDNA was prepared with the primer adapter of sequence 15' GAGAGAGAGATTCGACATGTAACATTAATATATTT modified cDNA was cleaved with XhoI and BamHI. Vector: a FIC I." 201 c 211 g 144 t

QY 880 CAGACCTTAAAGCTCCGTCAGTCGAGGACCTGCATGTCAACTTCAAGACATGGG 939
 DB 421 CAGAGACCTCAAGGCTCCGTCAGTCGAGGACCTGCATGTCAACTTCAAGACATGGG 480
 QY 940 CTGGAGACCTGATCATCGACCCCTTGAGTACGAGGCTTCCCTCGAGGGGCTGTG 999
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RESULT 13

BI084366

LOCUS 581 bp mRNA linear EST 20-JUN-2001
 DEFINITION 602869884F1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5014340 5',
 mRNA sequence.

ACCESSION

BI084366.1 GI:14502696

VERSION

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

NIH-MGC http://mgc.ncl.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cga@bbs-remail.nih.gov

FEATURES

Tissue Procurement: ATCC

SOURCE

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

FEATURES

DNA Sequencing by: Incyte Genomics, Inc.

SOURCE

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov

FEATURES

Plate: LICM1821 row: h column: 21

SOURCE

High quality sequence stop: 577.

FEATURES

Location/Qualifiers

SOURCE

1. 581

FEATURES

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SOURCE

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FEATURES

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SOURCE

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FEATURES

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SOURCE

/lab_host="DH10B (phage-resistant)"

FEATURES

/clone_id="NIH_MGC_102"

SOURCE

/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming,
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

BASE COUNT

110 a 173 c 201 g 97 t

FEATURES

source

FEATURES

1. 918

SOURCE

/organism="Homo sapiens"

FEATURES

/db_xref="taxon:9606"

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 DB 64 AAGCAGAGGTACGTTTGTGACATTTAGTCCCTGGAGAGAGATGGGCTCTGGGCGCAG 123
 QY 416 CTGCGGATCTTGGCGAAGAGCCCTCGGACACAGGCGCAAGCCAGCGGCCCGGAGCGGG 475
 DB 124 CTGCGGATCTTGGCGAAGAGCCCTCGGACACAGGCGCAAGCCAGCGGCCCGGAGCGGG 183
 QY 476 CGGGCTGCCACGCTGAGCTGTCCAGCTGCCCGCCAGCGGCCCGGAGCGGGCTCTGTG 535
 DB 184 CGGGCTGCCACGCTGAGCTGTCCAGCTGCCCGCCAGCGGCCCGGAGCGGGCTCTGTG 243
 QY 536 GATGTCGCTCCGTCGACGAGGCTGAGAGATCTGCTGGAGAGTCTTCGACATCTGAA 594
 DB 244 GATGTCGCTCCGTCGACGAGGCTGAGAGATCTGCTGGAGAGTCTTCGACATCTGAA 303
 QY 595 GCTCTTCGGAACCTTAAGAACTCGGCCAGCTGTGCTGAGAGCTGAGAGCTGGGAGACG 654
 DB 304 GCTCTTCGGAACCTTAAGAACTCGGCCAGCTGTGCTGAGAGCTGAGAGCTGGGAGACG 363
 QY 655 GGGCAGGCGCTGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 714
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 QY 715 GAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774
 DB 424 GAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483
 QY 775 TAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 834
 DB 484 TAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
 QY 835 AAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 869
 DB 544 AAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 578

RESULT 14

BI0854722/c

LOCUS

918 bp mRNA linear EST 16-OCT-2002

DEFINITION

AGENCOURT_10459020 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:6644065 5', mRNA sequence.

ACCESSION

BI0854722

VERSION

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

NIH-MGC http://mgc.ncl.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cga@bbs-remail.nih.gov

FEATURES

Tissue Procurement: ATCC

SOURCE

cDNA Library Arrayed by: Rubin Laboratory

FEATURES

DNA Sequencing by: Agencourt Bioscience Corporation

SOURCE

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov

FEATURES

Plate: LICM2879 row: b column: 01

SOURCE

High quality sequence start: 11

FEATURES

High quality sequence stop: 684.

SOURCE

Location/Qualifiers

FEATURES

1. 918

Query Match

46.4%; Score 559.8; DB 12; Length 581;

Best Local Similarity

99.5%; Pred. No. 3.1e-113;

Matches 572; Conservative

0; Mismatches 2; Indels 1; Gaps 1;

296 GCCAAGACCATCACCAGCTTTATTGACAAAGGCAAGATGACCGAGGTCCTGGTGCAGC 355

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/c1one_lib="NH_MCC.109"
/note="Organ: ovary; Vector: pORF7; Site:1: EcoRI; Site:2:
XhoI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
SuperScript II RT (Life Technologies). Note: this is a
NH_MCC Library."
BASE COUNT      202 a      256 c      277 g      179 t      4 others
ORIGIN

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Query Match      45.5%; Score 549.4; DB:13; Length 918;
Best Local Similarity 98.5%; Pred. No. 7.2e-111;
Matches 576; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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OY 684 GCTTGGAGCGGCGCG--CCCGGAGGTCCAGAGAGGCGCTGTTCCTGCTGTGGCGCG 742
DB 722 GCTTGGAGCGGCGCG--CCCGGAGGTCCAGAGAGGCGCTGTTCCTGCTGTGGCGCG 743
OY 743 ACCAAGAAAGGAGACCTGTTCTTAAATGAGATTAAAGCGCGCTGCGTGGCGAGAGATAG 802
DB 662 ACCAAGAAAGGAGACCTGTTCTTAAATGAGATTAAAGCGCGCTGCGTGGCGAGAGATAG 803
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DB 602 ACCGTGTAGAGTACCTGTTCAAGCGCGGCGGAAAGCGGCGCGCGCGCGCGCGCGCG 863
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DEFINITION 346810 MARC 1Prg Sus scrofa cDNA 5', mRNA sequence.
ACCESSION  Bg733101.1 GI:14019385
VERSION     Bg733101.1
KEYWORDS    EST.
SOURCE      Sus scrofa (p19)
ORGANISM    Sus scrofa
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE   1 (bases 1 to 571)
AUTHORS     Fahnenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,

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Vallat,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush
J., and Keele,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm Genome 13 (8), 475-478 (2002)
22213789
PUBMED
12226715
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
P.O. Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
V0.980904.e. Vector identified by cross-match with the -m1nscore 18
and -m1match 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
REVERSE: GTTTCACATCAGCAGC
Plate: 108 row: H column: 11
Seq primer: ATTAGGTGACTATAG.
Location/Qualifiers
1. 571

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FEATURES

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source

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BASE COUNT      110 a      173 c      188 g      100 t
ORIGIN

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Query Match      42.8%; Score 516.6; DB:10; Length 571;
Best Local Similarity 94.0%; Pred. No. 1.1e-103;
Matches 537; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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DB 121 GACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
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DB 241 AGGTGTCAGACATCTGGAAGCTTCTCGAAGCTTGAAGAGCGGCGGCGGCGGCGGCGG 240
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DB 301 CCGCCCGGAGGTCACAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 755
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Db	541	TGGGCTGGGATGACTGATTTATGCTCCCT	571

Search completed: August 28, 2003, 06:45:04
Job time : 2899 secs

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search, using sw model
search time 91 seconds

556C-1 1207

Scoring table: Gapop 10.0 / 220691566 residues 1139956

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Issued Patents NA:5A_COMB.seq:*
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SUMMARIES

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3	1207	100.0	2703	4	US-08-288-508C-1	Sequence 1, App1
4	1207	100.0	2703	4	US-09-180-700-4	Sequence 2, App1
5	1207	100.0	2703	4	US-08-981-490B-3	Sequence 3, App1
6	1207	100.0	2703	4	US-08-362-670B-3	Sequence 3, App1
7	1207	99.9	1207	3	US-08-333-576B-3	Sequence 3, App1
8	1205.4	99.9	1207	3	US-08-808-324-3	Sequence 9, App1
9	1205.4	99.9	1207	3	PCF-US94.14030A-5	Sequence 9, App1
10	1205.4	99.9	1207	5	US-08-455-559-9	Sequence 9, App1
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12	1039	86.1	2329	5	PCF-US94.00657-9	Sequence 25, App1
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14	1039	86.1	2329	5	US-08-362-670B-25	Sequence 25, App1
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[illegible]

RESULT 1
US-08-289-222E-1 Application US/08289224E
Sequence 1
Patent No. 6120760
GENERAL INFORMATION:
APPLICANT: HOTTEK, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
APPLICANT: GROWTH/DIFFERENTIATION FACTORS OF
TITLE OF INVENTION: FAMILY
TITLE OF INVENTION: 53
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAILO, MARCELSTEIN, MURRAY & ORAM
ADDRESS: 655 FIFTEENTH STREET, N. W., G STREET LOBBY
STREET: SUITE 330
STREET: WASHINGTON
CITY: DC
STATE: USA
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent/In Release #1.0, Version #1.25
SOURCE: APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/289,222E
APPLICATION NUMBER: 23-AUG-1999
FILING DATE: 424
CLASSIFICATION: DATA:
PRIOR APPLICATION NUMBER: US 08/289,222
APPLICATION NUMBER: 12-AUG-1994
FILING DATE: 12 DATA: DE P 44 23 190.3
PRIOR APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07 JUL-1994
APPLICATION NUMBER: EPO 92102324.8
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: EPO 92102324.8
APPLICATION NUMBER: 12-FEB-1992
FILING DATE: 12-FEB-1992
APPLICATION DATA: PCT/EP93/00350
PRIOR APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
APPLICATION NUMBER: 12-FEB-1993
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
NAME STRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
RECORDING/DOCKET INFORMATION:
TELECOMMUNICATION 1438-5000
TELEPHONE: 202/638-4810
TELEFAX: 202/638-4810
TELETYPE: 202/638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

Thu Aug 28 08:27:31 2003

us-09-901-556c-1.rni

Page 2

LENGTH: 1207 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: Linear
MOLECULE TYPE: DNA or cDNA from mRNA
US-08-289-222E-1

Query Match 100.0%; Score 1207; DB 3; Length 1207;
Best Local Similarity 100.0%; Pred. No. 3, 5e-266;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1201 CAGGTAG 1207

RESULT 2
US-09-054-526B-1
; Sequence 1, Application US/09054526B
; Patent No. 6197550
; GENERAL INFORMATION:
; APPLICANT: H TITEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054, 526B
; FILING DATE: 03-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289, 222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 01-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/POCKET NUMBER: P564-8005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA or cDNA from mRNA
US-09-054-526B-1

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Query Match      100.0%; Score 1207; DB 3; Length 1207;
Best Local Similarity 100.0%; Pred. No. 3, se-266;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 541 GCGCTCGGTCGCAAGGCTGTGAGAGATGCTGCTGGAGAGTGTTCACATCTGGAAGCT 600
OY 601 CCGAAACCTTTAAGAACTCGGCCAGCTGTGCTGAGAGCTGGAAGCGGAGGAG 660
DB 601 CCGAAACCTTTAAGAACTCGGCCAGCTGTGCTGAGAGCTGGAAGCGGAGGAG 660
OY 661 GGGCGTGAGACCTCGTGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 720
DB 661 GGGCGTGAGACCTCGTGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 720
OY 721 CCTGTTCTGCTGTTTGGGCGCCACCAAGAAACGGGAGCTGTCTTTAATGAGATTAG 780
DB 721 CCTGTTCTGCTGTTTGGGCGCCACCAAGAAACGGGAGCTGTCTTTAATGAGATTAG 780
OY 781 CCGCTCTGCGCAGAGCATAGACCGTATAGTACCTGTTTCAGCCAGCGCGGCAAAAC 840
DB 781 CCGCTCTGCGCAGAGCATAGACCGTATAGTACCTGTTTCAGCCAGCGCGGCAAAAC 840
OY 841 GCGGGGCGCCACTGCGCACTCGCCAGGCGCAAGCAAGCAAGCAAGCAAGCAAGCA 900
DB 841 GCGGGGCGCCACTGCGCACTCGCCAGGCGCAAGCAAGCAAGCAAGCAAGCAAGCA 900
OY 901 CAGTCGGAAGGCACTGATGTAACCTTCAAGAGCATGGGCTGGAGACGATGATCATCG 960
DB 901 CAGTCGGAAGGCACTGATGTAACCTTCAAGAGCATGGGCTGGAGACGATGATCATCG 960

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OY 961 ACCCTTGATGAGAGGCTTTCCACTGCGAGGAGGCTGTGCGAGTTCCTATGCGCTCCA 1020
DB 961 ACCCTTGATGAGAGGCTTTCCACTGCGAGGAGGCTGTGCGAGTTCCTATGCGCTCCA 1020
OY 1021 CCTGAGGCCCAAGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 CCTGAGGCCCAAGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
OY 1081 CACACACCCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
DB 1081 CACACACCCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
OY 1141 CTCTGCCAACAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
DB 1141 CTCTGCCAACAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
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RESULT 3

US-08-288-508C-1

; Sequence 1, Application US/08288508C

; Patent No. 5994094

; GENERAL INFORMATION:

; APPLICANT: H then, Gertrud

; APPLICANT: Neidhardt, Helge

; APPLICANT: Paulista, Michael

; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF

; TITLE OF INVENTION: THE TGF- FAMILY

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nikolaio, Marmelstein, Murray & Oram LLP

; STREET: 655 Fifteenth Street N.W. Suite 330

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-5701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/288,508C

; FILING DATE: 10-AUG-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 43 26 829.3

; FILING DATE: 10-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 44 18 222.8

; FILING DATE: 25-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 44 20 157.5

; FILING DATE: 09-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: JAHNS, Kristina M.

; REGISTRATION NUMBER: P-41,092

; REFERENCE/DOCKET NUMBER: P564-4019

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)638-5000

; TELEFAX: (202)638-4810

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2703 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-288-508C-1


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: TITLE: New growth/differentiation factor of the
:         tgf-beta familie.
: JOURNAL: Patent : WO 95/04819
: DATE: 16-02-1995
: SEQUENCE DESCRIPTION: SEQ ID NO: 4:
: US-09-180-700-4

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Query Match	100.0%;	Score 1207;	DB 4;	Length 2703;
Best Local Similarity	100.0%;	Pred. No. 4.2e-266;		
Matches 1207; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	ACGGGGGGGCGTGAACCCCAAGCCAGGACACCTTCCCAAAACAAGGCAAGGCTACAGCCG	60
Db	939	ACGGGGGGGCGCTGAACCCCAAGCCAGGACACCTTCCCAAAACAAGGCAAGGCTACAGCCG	998
QY	61	GACTGTGACCCCAAAAAGACGCTTCCCGAGGCAAGGACACCCCAAAAAGAGATCTGT	120
Db	999	GACTGTGACCCCAAAAAGACAGCTTCCCGAGGCAAGGACACCCCAAAAAGAGATCTGT	1058
QY	121	CCCCAGCTCCTTCTGTGTGAAGAAGGCGCAGGAGACCCGGGGCCCCACAGAGCCCAAGA	180
Db	1059	CCCCAGCTCTTCTCTGTGAAGAAGGCGCAGGAGACCCGGGGCCCCACAGAGCCCAAGA	1118
QY	181	GCGGTTTCGGCCACCCCCATCACACCCCAAGATACATGCTCTGTCTGTACAGAGAGCT	240
Db	1119	GCGGTTTCGGCCACCCCCATCACACCCCAAGATACATGCTCTGTCTGTACAGAGAGCT	1178
QY	241	GTCGAGTCTGTACAGAAAGGAGGCAACGACGCGTGAAATTGAGAGCTGTGCGCCAA	300
Db	1179	GTCGAGTCTGTACAGAAAGGAGGCAACGACGCGTGAAATTGAGAGCTGTGCGCCAA	1238
QY	301	CACCATACACAGCTTATGTGCAAAAGGGCAAGATGACCGAGTCCCGTGTACAGGAACA	360
Db	1239	CACCATACACAGCTTATGTGCAAAAGGGCAAGATGACCGAGTCCCGTGTACAGGAACA	1298
QY	361	GAGGTACGTTTGTACATTTAGTGTGCTGTGAAAGATGTGGCTGTGGGGGCGAGCTCG	420
Db	1299	GAGGTACGTTTGTACATTTAGTGTGCTGTGAAAGATGTGGCTGTGGGGGCGAGCTCG	1358
QY	421	GATCTTGGGGAAGAAAGCCCTTCGACACAGGCGCAAGCCAGCGGCCCCCGGAGCGGGCG	480
Db	1359	GATCTTGGGGAAGAAAGCCCTTCGACACAGGCGCAAGCCAGCGGCCCCCGGAGCGGGCG	1418
QY	481	TGCGCAGCTAAGCTGTGCAAGCTGCCAGCGCGGCGGCGAGCGGCGCTCTGTGCTGATGT	540
Db	1419	TGCGCAGCTAAGCTGTGCAAGCTGCCAGCGCGGCGGCGAGCGGCGCTCTGTGCTGATGT	1478
QY	541	GGCCTCGGTGCAGAGCCCTGACAGCATCTGGCTGGGAGTGTTCACATCTGGAAGCTCTT	600
Db	1479	GGCCTCGGTGCAGAGCCCTGACAGCATCTGGCTGGGAGTGTTCACATCTGGAAGCTCTT	1538
QY	601	CGAAGACTTTAAGAACTTCGGCCCAAGCTGTGCTTGAAGCTGGAGGCTTGGAAACGGGCGAG	660
Db	1539	CGAAGACTTTAAGAACTTCGGCCCAAGCTGTGCTTGAAGCTGGAGGCTTGGAAACGGGCGAG	1598
QY	661	GCGCGTGGACCTCGTGGGCTTTCGACCGGCGCCCGGCGAGGTCGACAGAAAGCG	720
Db	1599	GCGCGTGGACCTCGTGGGCTTTCGACCGGCGCCCGGCGAGGTCGACAGAAAGCG	1658
QY	721	CGTGTTCCTGTGTTTGGCCGACCAAGAAACGGGACCTGTCTTTAATGAGATTAAGGC	780
Db	1659	CGTGTTCCTGTGTTTGGCCGACCAAGAAACGGGACCTGTCTTTAATGAGATTAAGGC	1718
QY	781	CGCGCTCGGGCAGAGACATTAAGACCGGTGTATGATTACTGTTCAGGCCAGCGCGAAAGCG	840
Db	1719	CGCGCTCGGGCAGAGACATTAAGACCGGTGTATGATTACTGTTCAGGCCAGCGCGCGAAAGCG	1778
QY	841	GCGGGGCCCACTGGCCACTCGCCAGAGGCGCAAGCCAGCAAGAAACTTTAAGGCTCGCTG	900
Db	1779	GCGGGGCCCACTGGCCACTCGCCAGAGGCGCAAGCCAGCAAGAAACTTTAAGGCTCGCTG	1838
QY	901	CAGTCGGAAGCACTGATGTCAACTTTCAGAGCAATGGGCTGGAGCACTGGATCATCGC	960
Db		CAGTCGGAAGCACTGATGTCAACTTTCAGAGCAATGGGCTGGAGCACTGGATCATCGC	

Db	1839	CAGTCGGAAGGCACTGCATGTCACATCTTCACAGACATGGGCTGTGGAGCACTGGATCATCGC	1899
QY	961	ACCCCTTGAGTACGAGGCTTTCACATGCGAGAGGGCTGTGGCAGTTCCCATTTGGCGCTCCA	1020
Db	1899	ACCCCTTGAGTACGAGGCTTTCACATGCGAGAGGGGCTGTGGCAGTTCCCATTTGGCGCTCCA	1958
QY	1021	CGTGGAGCCCAAGCAATCATGCAGTGCATCCACACCCCTGATGTAACHTCCATGAGACCCCGAGTC	1088
Db	1959	CGTGGAGCCCAAGCAATCATGCAGTGCATCCACACCCCTGATGTAACHTCCATGAGACCCCGAGTC	2018
QY	1081	CACACCAACCCACCTGCTGTGTGTGCCACGCGGCTGAGTCCCATCAGCAATCCCTTATTGGA	1144
Db	2019	CACACCAACCCACCTGCTGTGTGTGCCACGCGGCTGAGTCCCATCAGCAATCCCTTATTGGA	2078
QY	1141	CTGTGCCCAACCAAGCTGTGTATTAAGCAGTATGAGAGACATGGTCTGGAGTGTGTGGCGTGTG	1200
Db	2079	CTGTGCCCAACCAAGCTGTGTATTAAGCAGTATGAGAGACATGGTCTGGAGTGTGTGGCGTGTG	2138
QY	1201	CAGGTAG 1207	
Db	2139	CAGGTAG 2145	

RESULT 5
US-08-981-490B-2
; Sequence 2, Application US/08981490B
; Patent No. 6531450

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: TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF
:
: TITLE OF INVENTION: NERVOUS SYSTEM
:
: FILE REFERENCE: 100564-07032
:
: CURRENT APPLICATION NUMBER: US/08/981,490B
:
: PRIOR FILING DATE: 1998-05-18
:
: PRIOR APPLICATION NUMBER: PCT/EP96/03065
:
: PRIOR FILING DATE: 1996-07-12
:
: PRIOR APPLICATION NUMBER: DE/195 25 416.3
:
: PRIOR FILING DATE: 1995-07-12
:
: NUMBER OF SEQ ID NOS: 7
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: SOFTWARE: Patentin version 3.1
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: LENGTH: 2703
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: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: (640)..(2142)
:
: OTHER INFORMATION:
:
: IS-08-981-490B-2

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Query Match	100.0%;	Score 1207;	DB 4;	Length 2703;
Best Local Similarity	100.0%;	Pred. No. 4.2e-266;		
Matches 1207; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	ACGGGGGGGGCCCTAAACCCAAAGCCAGGACACCTTCCCAAAACAAGGCGAGGGCTACAGCCCG	60
Db	939	ACGGGGGGGGCCCTTAACCCAAAGCCAGGACACCTTCCCAAAACAAGGCGAGGCTACAGCCCG	998
QY	61	GACTGTGACCCCAAAAGGACAGCTTCCCGAGGAGAAAGCACCCCAAAAGCAGATCTGT	120
Db	999	GACTGTGACCCCAAAAGGACAGCTTCCCGAGGAGCAAGCACCCCAAAAGCAGATCTGT	1055
QY	121	CCCCAGCTCCTCTGCTGTGAAGAAAGGCCAGGAGCCCGGGCCCCACAGAGAGCCCAAGGA	180
Db	1059	CCCCAGCTCCTCTGCTGTGAAGAAAGGCCAGGAGAGCCCGGGCCCCACAGAGAGCCCAAGGA	1111
QY	181	GCGGTTTCGGCCACCCCCCATCACACCCCAACGATGATCATGCTTTCGCTGTACAGAGAGCT	240
Db	1119	GCGGTTTCGGCCACCCCCCATCACACCCCAACGATGATCATGCTTTCGCTGTACAGAGAGCT	1178

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Page 6

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Db	1179	GTCCGATGCTGACAGAAAGGGGAGCAGACAGCTGAATTGAGAGCTGGCTGGCCAA	1238
OY	301	CACCAATCACCACTTTATTGACAAAGGGCAAGTACCCGAGTCCCTGTGTAGAGACGA	360
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OY	361	GAGGTACGTGTTTGACATTACTGCCCCGTGGAGAAAGATGGCTCTCTGGGGCCGACCTGC	420
Db	1299	GAGGTACGTGTTTGACATTACTGCCCCGTGGAGAAAGATGGCTCTCTGGGGCCGACCTGC	1358
OY	421	GATCTTGGCGAAGAAAGCCCTGGACAGGGCCAAAGCGGGCCCCCGAGAGCGAGCGAGC	480
Db	1359	GATCTTGGCGAAGAAAGCCCTGGACAGGGCCAAAGCGGGCCCCCGAGAGCGAGCGAGC	1418
OY	481	TGCCAGCTGAAGCTGTCCAGCTGGCCAGCGGGCCGAGCCGAGCTCTTCTGTGAATGT	540
Db	1419	TGCCAGCTGAAGCTGTCCAGCTGGCCAGCGGGCCGAGCCGAGCTCTTCTGTGAATGT	1478
OY	541	GGCCTCCGTGCACAGGCTGTGACAGGATCTGGCTGGAGAGTGTGACATCTGGAACTCTT	600
Db	1479	GGCCTCCGTGCACAGGCTGTGACAGGATCTGGCTGGAGAGTGTGACATCTGGAACTCTT	1538
OY	601	CCGAAACTTAAAGAACTGGGCCCAAGCTGTGCTGGACCTGGAGCCCTGGGAAACGGGGCAG	660
Db	1539	CCGAAACTTAAAGAACTGGGCCCAAGCTGTGCTGGACCTGGAGCCCTGGGAAACGGGGCAG	1598
OY	661	GGCCGCGAGACCTCCGTGGCTGGGGCTTGACACCGGCGCCCGGGCAGGTCCACAGAAAGC	720
Db	1599	GGCCGCGAGACCTCCGTGGCTGGGGCTTGACACCGGCGCCCGGGCAGGTCCACAGAAAGC	1658
OY	721	CGCTTCCCTGTGTTGTTGGCCGACCAAGAAACGGGACCTTCTTTAATGAGATTAAAGC	780
Db	1659	CGCTTCCCTGTGTTGTTGGCCGACCAAGAAACGGGACCTTCTTTAATGAGATTAAAGC	1718
OY	781	CGGCTTGGCCAGAGACGATTAAGACCGGTGTATGATTACTTTCAGCCAGCGGCGAAACG	840
Db	1719	CGGCTTGGCCAGAGACGATTAAGACCGGTGTATGATTACTTTCAGCCAGCGGCGAAACG	1778
OY	841	GGGGGCCCCACTGGCCACTCGCCAGGGCAGACGACCAGCAAGAACCTTAAAGCTCGCTG	900
Db	1779	GGGGGCCCCACTGGCCACTCGCCAGGGCAGACGACCAGCAAGAACCTTAAAGCTCGCTG	1838
OY	901	CAGTCGGAAGGACTGCTATGCTCAACTTCAAGAGACATGGGCTGGGACGATGTGATATGCG	960
Db	1839	CAGTCGGAAGGACTGCTATGCTCAACTTCAAGAGACATGGGCTGGGACGATGTGATATGCG	1898
OY	961	ACCCCTTGAGTACAGAGGCTTTCCACTGTGGAGGGGCTGGGATTTCCATTGCGCTCCA	1020
Db	1899	ACCCCTTGAGTACAGAGGCTTTCCACTGTGGAGGGGCTGGGATTTCCATTGCGCTCCA	1958
OY	1021	CTGGAGGCCAGGATCAATGACAGTCAATCCAGACCCCTGTATATATCCATGAGACCCGAGTC	1080
Db	1959	CTGGAGGCCAGGATCAATGACAGTCAATCCAGACCCCTGTATATATCCATGAGACCCGAGTC	2018
OY	1081	CAGACACACCACTCTCTGTGTGCCACAGCGGCTGTAGTCCATATCAGCATCTCTTATATGA	1140
Db	2019	CAGACACACCACTCTCTGTGTGCCACAGCGGCTGTAGTCCATATCAGCATCTCTTATATGA	2078
OY	1141	CTCTGCCAACAAACGTGTGTATTAAGCAGATGAGAGACATGTGCTGGAGTCTGTGTGCTG	1200
Db	2079	CTCTGCCAACAAACGTGTGTATTAAGCAGATGAGAGACATGTGCTGGAGTCTGTGTGCTG	2138
OY	1201	CAGGTAG 1207	
Db	2139	CAGGTAG 2145	

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: Patent NO. 5658882
: GENERAL INFORMATION:
: APPLICANT: Celeste, Anthony J.
: APPLICANT: Mooney, John
: APPLICANT: Rosen, Vicki A.
: APPLICANT: Wolfman, Neil
: APPLICANT: Thomsen, Gerald H.
: APPLICANT: Melton, Douglas A.
: TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: GENETICS INSTITUTE, INC.
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/362,670B
: FILING DATE: December 22, 1994
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Lazar, Steven R.
: - REGISTRATION NUMBER: 32,618
: REFERENCE/DOCKET NUMBER: 5202-D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617 498-8260
: TELEFAX: 617 876-5851
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1207 base pairs
: TYPE: nucleic acid
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: CLONE: MP52
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 845..1204
: US-08-362-670B-3

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RESULT 6
US-08-362-670B-3
; Sequence 3, Application US/08362670B

Query Match	99.9%	Score 1205.4	DB 1	Length 1207
Best Local Similarity	99.9%	Pred. No. 8e-266		
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Db	1	ACCGGGGGGGCCCTGAACCCCAAGCCGAGACCTCTCCCAACAAAGCAGAGCTACAGCCG	60	
QY	61	GACTGTGACCCCAAAAGAGCAGCTCTCCGGAGGGCAAGGACCCCAAAAGCAGAGTCTGT	120	
Db	61	GACTGTGACCCCAAAAGAGCAGCTCTCCGGAGGGCAAGGACCCCAAAAGCAGAGTCTGT	120	
QY	121	CCCCACTCTCTTCGTCTGAAGAAAGGCCAGGAGACCCGGGCCCCACAGAGACCCCAAGA	180	
Db	121	CCCCACTCTCTTCGTCTGAAGAAAGGCCAGGAGACCCGGGCCCCACAGAGACCCCAAGA	180	
QY	181	GCCGTTTGCCCAACCCCCATCAACACCCACAGATACATGCTCTCGCTGTACAGAGCGT	240	
Db	181	GCCGTTTGCCCAACCCCCATCAACACCCACAGATACATGCTCTCGCTGTACAGAGCGT	240	
QY	241	GTCGAGTGTGACAGAAAGCAGAGCAGCAGCTGAAGTTGAGAGCTGGCCCTGACC	300	
Db	241	GTCGAGTGTGACAGAAAGCAGAGCAGCAGCTGAAGTTGAGAGCTGGCCCTGACC	300	

OY 301 CACCATCACACCTTTATTGACAAAGGGCAGATACCGAGGTCCCGTGTGACGAGCA 360
 DB 301 CACCATCACACCTTTATTGACAAAGGGCAGATACCGAGGTCCCGTGTGACGAGCA 360
 OY 361 GAGGTACCTGTTGACATTAGTGCCTCGAGAGAGATGGGCTGTGGGGGCCGAGCTGG 420
 DB 361 GAGGTACCTGTTGACATTAGTGCCTCGAGAGAGATGGGCTGTGGGGGCCGAGCTGG 420
 OY 421 GATCTGGGGAAGAGCCCTCGGACACGCGCCAGCCGCGCCCGGAGGCGGCGGCG 480
 DB 421 GATCTGGGGAAGAGCCCTCGGACACGCGCCAGCCGCGCCCGGAGGCGGCGGCG 480
 OY 481 TGCCAGCTGAAGCTGTCCAGCTGCCCCAGCGCGCGCGAGCCGCGCTCTGTGATGT 540
 DB 481 TGCCAGCTGAAGCTGTCCAGCTGCCCCAGCGCGCGCGAGCCGCGCTCTGTGATGT 540
 OY 541 GCGCTCGGTGCGAGGCTGTGAGCGGATGTGGGAGGTGTGCAATCTGGAACCTCTT 600
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 OY 601 CCGAATCTTAAAGACTGCGCCAGCTGTGCTGAGCTGAGGCTGAGGAGGAGGCGAG 660
 DB 601 CCGAATCTTAAAGACTGCGCCAGCTGTGCTGAGCTGAGGCTGAGGAGGAGGCGAG 660
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 OY 721 CCGTTCCTGAGTGTGGCGCGACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
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 OY 901 CAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
 DB 901 CAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
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 DB 961 ACCCTTGAAGTACGAGGCTTTCACACTGCGAGGAGGAGGAGGAGGAGGAGGAGG 1020
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 DB 1081 CAC 1140
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 DB 1141 CTCTGCGCAACACGCTGTATATGACAGTATGAGGAGGAGGAGGAGGAGGAGGAG 1200
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 DB 1201 CAGGTAG 1207

RESULT 7
 ; Sequence 3, Application US/08333576C
 ; Patent No. 6027919
 ; GENERAL INFORMATION:
 ; APPLICANT: Celeste, Anthony J.
 ; APPLICANT: Mooney, John
 ; APPLICANT: Rosen, Vicki A.

APPLICANT: Woliman, Neil
 APPLICANT: Thomson, Gerald H.
 APPLICANT: Melton, Douglas A.
 TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333,576C
 FILING DATE: No. 6027919, September 2, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REGISTRATION NUMBER: 32,618
 REFERENCE/DOCKET NUMBER: 5202-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498-8260
 TELEFAX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1207 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: MP52
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 845..1204
 US-08-333-576C-3
 Query Match 99.9%; Score 1205.4; DB 3; Length 1207;
 Best Local Similarity 99.9%; Pred. No. 86-266;
 Matches 1206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACCGGGGGCGCCCTGGAACCCAGACGACACCCCTCCCAAAACAGGCGATACAGCCCG 60
 DB 1 ACCGGGGGCGCCCTGGAACCCAGACGACACCCCTCCCAAAACAGGCGATACAGCCCG 60
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 DB 61 GACTGTGACCCCAAAAGGACAGCTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGG 120
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 OY 181 GCGGTTTGGCCACCCCCCATACACCCCGAGAGTACATGCTGCTGTGTACAGAGCGT 240
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 OY 241 GTCCGATGCTGACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
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 OY 301 CACCATCACACCTTTATTGACAAAGGGCAGATACCGAGGTCCCGTGTGACGAGCA 360
 DB 301 CACCATCACACCTTTATTGACAAAGGGCAGATACCGAGGTCCCGTGTGACGAGCA 360
 OY 361 GAGGTACCTGTTGACATTAGTGCCTCGAGAGAGATGGGCTGTGGGGGCCGAGCTGG 420

Db 361 GAGGTACGCTTTGACCTTATGAGTCCCTGGAGAAAGATGGCTCTGGGGGCCGAGCTCCG 420
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Db 421 GATCTTGGGAAAGAGCCCTGCGACACAGCCAGCCAGCCGCGCCGCGAGGCGGCGGCG 480
Qy 481 TGCCCAAGCTGAAGCTGCTCCAGCTGCGCCAGCCGCGCCGCGAGCCCTGCTGGATGT 540
Db 481 TGCCCAAGCTGAAGCTGCTCCAGCTGCGCCAGCCGCGCCGCGAGCCCTGCTGGATGT 540
Qy 541 GCGCTCCGTGGCCAGCGCTGAGAGGATGCTGGCTGGAGGCTGGATGATGAGAGCTTT 600
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Qy 721 CCTGTTCCTGCTGTTGGCGCGACCAAGAAAGGAGGAGCTTTTAAATGAGATTAAAGC 780
Db 721 CCTGTTCCTGCTGTTGGCGCGACCAAGAAAGGAGGAGCTTTTAAATGAGATTAAAGC 780
Qy 781 CCGCTCTGGCGAGAGATGAAGCGGTATGAGTACTGTTACCCAGCCGCGGAAAGC 840
Db 781 CCGCTCTGGCGAGAGATGAAGCGGTATGAGTACTGTTACCCAGCCGCGGAAAGC 840
Qy 841 GCGGCGCCGCGAGCTGCGCGAGAGCGAGAGCCGCGGAAAGCTTAAAGCTGCTG 900
Db 841 GCGGCGCCGCGAGCTGCGCGAGAGCGAGAGCCGCGGAAAGCTTAAAGCTGCTG 900
Qy 901 CAGTGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 CAGTGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy 961 ACCCTTGTAGTACAGAGCTTTCACCTGCGAGAGGCTGCGAGTGTCCCATTTGCGCTGCA 1020
Db 961 ACCCTTGTAGTACAGAGCTTTCACCTGCGAGAGGCTGCGAGTGTCCCATTTGCGCTGCA 1020
Qy 1021 CCTGAGAGCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 CCTGAGAGCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Qy 1081 CACACGACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 CACACGACCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Qy 1141 CTCTGCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 CTCTGCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Qy 1201 CAGGTAG 1207
Db 1201 CAGGTAG 1207

Correspondence Address:
ADDRESS: GENNETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: Homo sapiens
IMMEDIATE SOURCE: MP52
FEATURE:
NAME/KEY: CDS
LOCATION: 845..1204
US-08-808-324-3

Query Match 99.9%; Score 1205.4; DB 3; Length 1207;
Best Local Similarity 99.9%; Pred. No. 8e-266; Matches 1206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACCGGGCGGCGCTGAGAACCCAGCCAGAGCACCCTCCCAAAAGAGGCTACAGCCCG 60
Db 1 ACCGGGCGGCGCTGAGAACCCAGCCAGAGCACCCTCCCAAAAGAGGCTACAGCCCG 60
Qy 61 GACTGTGACCCCAAAAGAGACAGCTTCCCGAGAGGACACCCCAAAAGAGGATCTGT 120
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Qy 121 CCCAGACTCTCTCTGCTGTAAGAAAGGCGAGAGGCGCGGCGCCCAAGAGGCGCAAGA 180
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Qy 181 GCGGTTTGCGCCACCCCATACACCCCGAGAGTACATGCTGCTGCTGTAAGAGAGCT 240
Db 181 GCGGTTTGCGCCACCCCATACACCCCGAGAGTACATGCTGCTGCTGTAAGAGAGCT 240
Qy 241 GTCCGATCTGACAGAAAGGAGGAGCAACAGCAGCTGAAGTGAAGGCTGGCTGGCCAA 300
Db 241 GTCCGATCTGACAGAAAGGAGGAGCAACAGCAGCTGAAGTGAAGGCTGGCTGGCCAA 300
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Db 301 CACCATCACAGCTTTATTGACAAAGGAGCAAGATGACCCGAGAGTCCGTGTCAGAAAGCA 360
Qy 361 GAGGTACGCTGTTTACATTAAGTGGCTGAGAGAGATGGCTGCGGGGCGAGCTGGCG 420
Db 361 GAGGTACGCTGTTTACATTAAGTGGCTGAGAGAGATGGCTGCGGGGCGAGCTGGCG 420
Qy 421 GATCTTGGGAAAGAGCCCTGCGACACAGCCAGCCAGCCGCGCCGCGAGGCGGCGGCG 480

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Db 421 GATCTGGGGAAGAGCCCTGGGACAGCGCCCAAGCCAGCGGCCCGCCGAGCGGCG 480
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Db 481 TGCCAGCTGAAGCTGTCCAGCTGCGCCAGCGGCGCGGAGCGCGGCTCTGCTGGAGT 540
Qy 541 GCGCTCCCTGGCAGGCTGAGAGGATCTGGCTGGAGGCTGTTCCAGATCTGGAGCTCTT 600
Db 541 GCGCTCCCTGGCAGGCTGAGAGGATCTGGCTGGAGGCTGTTCCAGATCTGGAGCTCTT 600
Qy 601 CCGAAGCTTTAAGAACTGCGGCGGAGCTGGCTGGAGGCTGGAGGCTGGAGGCGGAG 660
Db 601 CCGAAGCTTTAAGAACTGCGGCGGAGCTGGCTGGAGGCTGGAGGCTGGAGGCGGAG 660
Qy 661 GCGCGTGGACCTCCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 720
Db 661 GCGCGTGGACCTCCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 720
Qy 721 CCTGTTCTGCTGTTGTTGGCCGACCAAGAAACGGGAGCTGTTTAAATGAGATTAGGC 780
Db 721 CCTGTTCTGCTGTTGTTGGCCGACCAAGAAACGGGAGCTGTTTAAATGAGATTAGGC 780
Qy 781 CCGCTGCGGCGAGGAGATGAGAGCGGTGATGATGATGATGATGATGATGATGATGAT 840
Db 781 CCGCTGCGGCGAGGAGATGAGAGCGGTGATGATGATGATGATGATGATGATGATGAT 840
Qy 841 GCGGCGCCCACTGGCTGCTGGCGAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 900
Db 841 GCGGCGCCCACTGGCTGCTGGCGAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 900
Qy 901 CAGTGGGAAGGACATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 960
Db 901 CAGTGGGAAGGACATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 960
Qy 961 ACCCTTGATGAGGAGGCTTCCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db 961 ACCCTTGATGAGGAGGCTTCCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Qy 1021 CCTGAGGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1021 CCTGAGGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Qy 1081 CACACACCCACCTGCTGTGTGCGCAGCGGCTGAGTCCATGACATCTCTTATGTA 1140
Db 1081 CACACACCCACCTGCTGTGTGCGCAGCGGCTGAGTCCATGACATCTCTTATGTA 1140
Qy 1141 CTCGCGCCAAACGCTGTGTGTATGAGCATATGAGAGCATGCTGTGTGTGTGTG 1200
Db 1141 CTCGCGCCAAACGCTGTGTGTATGAGCATATGAGAGCATGCTGTGTGTGTGTG 1200
Qy 1201 CAGGTAG 1207
Db 1201 CAGGTAG 1207

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RESULT 9

PCT-US94-14030A-3
Sequence 3, Application PC/TUS9414030A

GENERAL INFORMATION:

APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202D-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: MP52
FEATURE:
NAME/KEY: CDS
LOCATION: 845..1204
PCT-US94-14030A-3

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Query Match 99.9%; Score 1205.4; DB 5; Length 1207;
Best Local Similarity 99.9%; Pred. No. 86-266;
Matches 1206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 ACCGGGGGCGCTGTGAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
Db 1 ACCGGGGGCGCTGTGAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
Qy 61 GACTGTGACCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db 61 GACTGTGACCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
Qy 121 CCCGAGCTCTCTCTGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 121 CCCGAGCTCTCTCTGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Qy 181 GCGGTTTGGCCACCCCATACACCCAGAGTATGCTGTGCTGTACAGAGAGCT 240
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Qy 241 GTCCGATGCTGACAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
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Qy 301 CACATACACACAGCTTATTGACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
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Qy 361 GAGGTACGTTGATGATTTAGTCCCTGGAGAGAGATGGCTGTGGGGGCGAGCTGG 420
Db 361 GAGGTACGTTGATGATTTAGTCCCTGGAGAGAGATGGCTGTGGGGGCGAGCTGG 420
Qy 421 GATCTGGGGAAGAGCCCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Db 421 GATCTGGGGAAGAGCCCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Qy 481 TGCCAGCTGAAGCTGTCCAGCTGCGCCAGCGGCGCGGAGCGCGGCTCTGCTGGAGT 540

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Thu Aug 28 08:27:31 2003

us-09-901-556c-1.rni

Page 10

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Db	601	CCGAAACTTTAAGAACTGGGCCACACTGCTGGCTGGAGTGGAGGCTGGGAAAGGGGCAAG	660
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OY	721	CGCTTCCGAGTGTGGGCTGGCCGACCAAGAAACGGAGCTGCTCTTAAATAGATTTAAGGC	780
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Db	781	CGCCTTGGCCAGAGAGATAGACCGCTGTATGATCTCTTACGCCAGCGCGGAAAGCG	840
OY	841	GGGGGCCCCACTGGCCACTCGCCAGGAGGCAAGCCAGCAAGAACTTAAAGCTCGCTG	900
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OY	901	CAGTCGGAAGGACATGCATATGTCATCTTCAAGAGACATGGGCTGGAGACATGCATATCCG	960
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OY	961	ACCCCTTGGATACGAGGCTTTCACATCTGGAGGGGCTGGAGATGCCATATGGGCTGCCA	1020
Db	961	ACCCCTTGGATACGAGGCTTTCACATCTGGAGGGGCTGGAGATGCCATATGGGCTGCCA	1020
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OY	1081	CACACCAACCACCTCTGTGTGCCACAGCGGCTATGATGCCATATGATCAATCTCTCTTCAATTA	1144
Db	1081	CACACCAACCACCTCTGTGTGCCACAGCGGCTATGATGCCATATGATCAATCTCTCTTCAATTA	1144
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Db	1141	CTGTGGCAACAACTGTGTGTATATAGCACTATGAGGACATGTCTGTGAGTCTGTGTGGCTG	1200
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Db	1201	CAGGTAG 1207	

US-RESULT 10
US-08-455-559-9
Sequence 9, Application US/08455559
Patent No. 5801014
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLER HORN JUBAS & LUBITZ
STREET: 1880 COUNTRY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/455,559
3 FILING DATE: 31-MAY-1995
4 CLASSIFICATION: 435
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 08/003,144
7 FILING DATE: 12-JAN-1993
8 ATTORNEY/AGENT INFORMATION:
9 NAME: WETHERELL, JR. PH.D., JOHN R.
10 REGISTRATION NUMBER: 31,676
11 REFERENCE/DOCKET NUMBER: P02280
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 619/455-5100
14 TELEFAX: 619-455-5110
15 INFORMATION FOR SEQ. ID NO.: 9:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 2329 base pairs
18 TYPE: nucleic acid
19 STRANDEDNESS: single
20 TOPOLOGY: linear
21 MOLECULE TYPE: DNA (genomic)
22 IMMEDIATE SOURCE:
23 CLONE: GD-5
24 FEATURE:
25 NAME/KEY: CDS
26 LOCATION: 322..1807
27 US-08-455-559-9

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Query Match	Similarity	86.1% 91.3% Matches 1102;	Score 1039; Pred. No. 7.5e-228; 0; Mismatches 105;	DB 1; Length 2329; Indels 0;	Gaps 0;
QY	1	ACCGGCGGCGCTGTAACCCAGCCAGACACCTCCGCCAACAAGCGAGCTTACAGCCG	60		
Db	603	ATCCGGTGGCTGTGAACCCAGCCAGACGACCTCTTCCCACTAGACAGCGTGCACGCCG	662		
QY	61	GACTGTGACCCCAAAAGGACAGCTTCCCGGAGCCAGCACCCCAAAAGCAGATCTGT	120		
Db	663	GACTGTGACCCCAAAAGGACAGCTTCCGGGGGCAAAAGCATCTTCAAAAGCAGATCTGC	722		
QY	121	CCCGACCTTCCTTCGTGTGAAGAGCGCCAGGACCCCGGCGCCCAAGACCCCAAGA	180		
Db	723	CCCGACCTCTTCTGTGTGAAGAGCACAGGAGACCTGGGAGCCCTCGAGACCCCAAGA	782		
QY	181	GCGGTTGGCCACCCCGCATCACACCCACAGAGTATACCTCTGCTGTAGAGAGCT	240		
Db	783	GCGGTTGGCCCGCCCGCATCACACCCACAGATATACCTCTTCCCTGTAGAGAGCT	842		
QY	241	GTCGCACTGTGCACAAAGGAGGACCAACAGAGTGAATTGAGAGCTGGCTGGCCAA	300		
Db	843	GTCCGAGCTGTGCACAAAGGAGGTAAACAGAGGTGATGATTTGAGAGCTGGCTGGCCAA	902		
QY	301	CACCATACCAAGCTTTATTTGACAAAAGGCAAGATGACCGAGTCCCGTGTGAGGAACA	360		
Db	903	CACCATACCAAGCTTTATTTGACAAAAGGCAAGATGACCGAGGCTCGCGTCAAGGAACA	962		
QY	361	GAGGTACGTTTGCATTACTGCCCTGAGGAAGATGGGCTGCTGGGGCGGACCTCG	420		
Db	963	GAGGTACGTTTGCATTACTATGCTCTTGGAAAGATGGGCTGTGGGGCTGGAACCTCG	1022		
QY	421	GATCTTGGGGAAGAAAGCCCTCGGACACGGGCAAGCCAGCGGCCCGGAGGGGGCGGAC	480		
Db	1023	GATCTTACGGAAGAAAGCCCTTGGACGTGGCCAAACCAAGCGCTGTCCAGTATGGGGCGGGT	1082		
QY	481	TGCGCAGCTGAAGCTGTCCACAGCTCCCAAGCGGCGGCAAGCGGCGCTCTTGTGTGATGT	540		
Db	1083	TGCGCAACTGAAGCTGTCCACAGCTCCCAAGGGGCGGCAAGCGGCGCTTGTGTGAATGT	1142		
QY	541	GGCGTCCGTGCGAGGCTGACGAGTCTGGCTGGAGAGTGTTCGACATCTGGACACTCTT	600		
Db	1143	GGCGTCCGTGCGAGGCTGATGTGATCTGGCTGGAGAGTGTTCGACATCTGGACACTCTT	1202		
QY	601	CCGAAACTTTAAGAACTGGCGCAGCTGCTCGTGAAGCTGGAAGGCGCTGGGAACGGGGAG	660		

us-09-901-556c-1.rn1

1262 1261 1260 1259 1258 1257 1256 1255 1254 1253 1252 1251 1250 1249 1248 1247 1246 1245 1244 1243 1242 1241 1240 1239 1238 1237 1236 1235 1234 1233 1232 1231 1230 1229 1228 1227 1226 1225 1224 1223 1222 1221 1220 1219 1218 1217 1216 1215 1214 1213 1212 1211 1210 1209 1208 1207 1206 1205 1204 1203 1202 1201 1200 1199 1198 1197 1196 1195 1194 1193 1192 1191 1190 1189 1188 1187 1186 1185 1184 1183 1182 1181 1180 1179 1178 1177 1176 1175 1174 1173 1172 1171 1170 1169 1168 1167 1166 1165 1164 1163 1162 1161 1160 1159 1158 1157 1156 1155 1154 1153 1152 1151 1150 1149 1148 1147 1146 1145 1144 1143 1142 1141 1140 1139 1138 1137 1136 1135 1134 1133 1132 1131 1130 1129 1128 1127 1126 1125 1124 1123 1122 1121 1120 1119 1118 1117 1116 1115 1114 1113 1112 1111 1110 1109 1108 1107 1106 1105 1104 1103 1102 1101 1100 1099 1098 1097 1096 1095 1094 1093 1092 1091 1090 1089 1088 1087 1086 1085 1084 1083 1082 1081 1080 1079 1078 1077 1076 1075 1074 1073 1072 1071 1070 1069 1068 1067 1066 1065 1064 1063 1062 1061 1060 1059 1058 1057 1056 1055 1054 1053 1052 1051 1050 1049 1048 1047 1046 1045 1044 1043 1042 1041 1040 1039 1038 1037 1036 1035 1034 1033 1032 1031 1030 1029 1028 1027 1026 1025 1024 1023 1022 1021 1020 1019 1018 1017 1016 1015 1014 1013 1012 1011 1010 1009 1008 1007 1006 1005 1004 1003 1002 1001 1000 999 998 997 996 995 994 993 992 991 990 989 988 987 986 985 984 983 982 981 980 979 978 977 976 975 974 973 972 971 970 969 968 967 966 965 964 963 962 961 960 959 958 957 956 955 954 953 952 951 950 949 948 947 946 945 944 943 942 941 940 939 938 937 936 935 934 933 932 931 930 929 928 927 926 925 924 923 922 921 920 919 918 917 916 915 914 913 912 911 910 909 908 907 906 905 904 903 902 901 900 899 898 897 896 895 894 893 892 891 890 889 888 887 886 885 884 883 882 881 880 879 878 877 876 875 874 873 872 871 870 869 868 867 866 865 864 863 862 861 860 859 858 857 856 855 854 853 852 851 850 849 848 847 846 845 844 843 842 841 840 839 838 837 836 835 834 833 832 831 830 829 828 827 826 825 824 823 822 821 820 819 818 817 816 815 814 813 812 811 810 809 808 807 806 805 804 803 802 801 800 799 798 797 796 795 794 793 792 791 790 789 788 787 786 785 784 783 782 781 780 779 778 777 776 775 774 773 772 771 770 769 768 767 766 765 764 763 762 761 760 759 758 757 756 755 754 753 752 751 750 749 748 747 746 745 744 743 742 741 740 739 738 737 736 735 734 733 732 731 730 729 728 727 726 725 724 723 722 721 720 719 718 717 716 715 714 713 712 711 710 709 708 707 706 705 704 703 702 701 700 699 698 697 696 695 694 693 692 691 690 689 688 687 686 685 684 683 682 681 680 679 678 677 676 675 674 673 672 671 670 669 668 667 666 665 664 663 662 661 660 659 658 657 656 655 654 653 652 651 650 649 648 647 646 645 644 643 642 641 640 639 638 637 636 635 634 633 632 631 630 629 628 627 626 625 624 623 622 621 620 619 618 617 616 615 614 613 612 611 610 609 608 607 606 605 604 603 602 601 600 599 598 597 596 595 594 593 592 591 590 589 588 587 586 585 584 583 582 581 580 579 578 577 576 575 574 573 572 571 570 569 568 567 566 565 564 563 562 561 560 559 558 557 556 555 554 553 552 551 550 549 548 547 546 545 544 543 542 541 540 539 538 537 536 535 534 533 532 531 530 529 528 527 526 525 524 523 522 521 520 519 518 517 516 515 514 513 512 511 510 509 508 507 506 505 504 503 502 501 500 499 498 497 496 495 494 493 492 491 490 489 488 487 486 485 484 483 482 481 480 479 478 477 476 475 474 473 472 471 470 469 468 467 466 465 464 463 462 461 460 459 458 457 456 455 454 453 452 451 450 449 448 447 446 445 444 443 442 441 440 439 438 437 436 435 434 433 432 431 430 429 428 427 426 425 424 423 422 421 420 419 418 417 416 415 414 413 412 411 410 409 408 407 406 405 404 403 402 401 400 399 398 397 396 395 394 393 392 391 390 389 388 387 386 385 384 383 382 381 380 379 378 377 376 375 374 373 372 371 370 369 368 367 366 365 364 363 362 361 360 359 358 357 356 355 354 353 352 351 350 349 348 347 346 345 344 343 342 341 340 339 338 337 336 335 334 333 332 331 330 329 328 327 326 325 324 323 322 321 320 319 318 317 316 315 314 313 312 311 310 309 308 307 306 305

RESULT 11-05-06-9 application US/09145060
US-09-145-060-9
Sequence No. 6243896
PATENT INFORMATION:
APPLICANT: Lee, Se-Jin
INVENTOR: Huh, Thach
TITLE OF INVENTION: 27
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: 425 Executive Square, Suite 1400
STREET: La Jolla
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTIO for Windows Version 2.0
CURRENT APPLICATION DATA:
SOURCING APPLICATION DATA: US/09/145,060
APPLICATION NUMBER:
FILING DATE:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
PRIORITY APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Hall, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET INFORMATION: 07265/057001
RECOMMUNICATION TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5099
ID NO: 9
INFORMATION FOR SEQ. ID NO: 9:
INFORMATION CHARACTERISTICS:
SEQUENCE LENGTH: 2329 base pairs
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
IMMEDIATE SOURCE: clone: GD-5
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 322...1806
DB 3; Length 2329;
Score 1039; 5e-226;
Pred. No. gaps 0;
Indels 0;
Gaps 0;
Indels 60

Query Match	Similarity	91.3%	0	Mismatches
Best local	1102:	Conservative		
Matches	1102:			
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603	ATCCGGTGGCTTGAACCAAGCAGAGACCTCTTCCCAACTAGCAGAGCTGACGCCG			662
603	ATCCGGTGGCTTGAACCAAGCAGAGACCTCTTCCCAACTAGCAGAGCTGACGCCG			722
61	GACTGTGACCCAAAGAGAGAGCTCCGAGGAGAGACACCCCAAAAGCAGATCTGT			120
61	GACTGTGACCCAAAGAGAGAGCTCCGAGGAGAGACACCCCAAAAGCAGATCTGT			180
663	GACTGTGACCCAAAGAGAGAGCTCCGAGGAGAGACACCCCAAAAGCAGATCTGT			782
121	CCCCAGCTCTTCCTGCTGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG			240
723	CCCCAGCTCTTCCTGCTGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG			842
181	GCGCTTTGGCCCAACCCCAACACACCCAGAGAGAGAGAGAGAGAGAGAGAGAG			300
783	GCGCTTTGGCCCAACCCCAACACACCCAGAGAGAGAGAGAGAGAGAGAGAGAG			902
241	GTCGAGTGTGTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG			360
843	GTCGAGTGTGTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG			962
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661	GCGCTGAGAGCTGAG			
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Thu Aug 28 08:27:31 2003

us-09-901-556c-1.rni

Page 12

US -

721 CCGTTCCTGGTGTGTTGGCCGACCAAGAAAGGACCTGTTCTTTATATGATTAAGC 780
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Db 1323 CTGTGTTCCCTAGTGTGTTGGTCTGTACCAAGAAACCGAGACGTTCTTTATATGATTAAGC 780
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OY 1201 CAGGTAG 1207
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Db 1803 CAGGTAG 1809

RESULT 12
PCT-US94/00657-9
Sequence 9, Application PC/TUS94/00657
GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
TITLE OF INVENTION: HUYNH, THANH
NUMBER OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
CORESPONDENCE SEQUENCES: 27
ADDRESS: ADDRESS:
STREET: SPENSLER
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: CALIFORNIA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
CREATING SYSTEM: IBM PC compatible
SOFTWARE: Patencl Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER DATA:
FILING DATE: 1/12/94
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
TELECOMM/DOCKET NUMBER: FD3256 CIP OF PD2280
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2339 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 04:33:30 ; Search time 344 Seconds
(without alignments)
8049.886 Million cell updates/sec

Title: US-09-901-556C-1

Perfect score: 1207

Sequence: 1 accggcgccctgaaccca.....agtcgtgtgctgcagtag 1207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1533700 seqs, 1147125425 residues 3067400

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1207	100.0	2703	8 US-08-981-490B-2	Sequence 2, Appl1
2	1205.4	99.9	1207	10 US-09-945-182-3	Sequence 3, Appl1
3	1191	98.7	2341	9 US-09-730-772-11	Sequence 11, Appl1
4	1191	98.7	2341	9 US-09-735-849-11	Sequence 11, Appl1
5	1039	86.1	2329	10 US-09-880-708-9	Sequence 9, Appl1
6	355.4	29.4	357	10 US-08-945-459A-4	Sequence 4, Appl1
7	355.4	29.4	357	10 US-09-068-253-1	Sequence 1, Appl1
8	334.6	27.7	599	9 US-09-864-761-6620	Sequence 6620, Appl1
9	251.6	20.8	1171	10 US-09-945-182-25	Sequence 25, Appl1
10	242.8	20.1	1308	9 US-09-730-772-12	Sequence 12, Appl1
11	242.8	20.1	1308	9 US-09-735-849-12	Sequence 12, Appl1
12	238	19.7	1046	10 US-09-945-182-11	Sequence 12, Appl1
13	214.4	17.8	475	10 US-09-833-381-582	Sequence 582, Appl1
14	214.4	17.8	926	10 US-09-945-182-1	Sequence 1, Appl1
15	214.4	17.8	1345	10 US-09-945-182-33	Sequence 33, Appl1
16	214.4	17.8	1447	14 US-10-188-246-11	Sequence 11, Appl1

17	212.8	17.6	272	10 US-09-945-182-14	Sequence 14, Appl1
18	212.8	17.6	1203	10 US-09-945-182-29	Sequence 29, Appl1
19	212.2	17.6	3585	10 US-09-945-182-9	Sequence 9, Appl1
20	211.4	17.5	1233	10 US-09-945-182-27	Sequence 27, Appl1
21	177.6	14.7	272	10 US-09-945-182-12	Sequence 12, Appl1
22	176	14.6	272	10 US-09-945-182-10	Sequence 10, Appl1
23	165	13.7	165	9 US-09-864-761-23354	Sequence 23354, A
24	139	11.5	557	9 US-09-765-527-248	Sequence 248, Appl1
25	139	11.5	1004	8 US-08-957-425-10	Sequence 1, Appl1
26	139	11.5	1277	8 US-08-957-425-14	Sequence 10, Appl1
27	139	11.5	1505	8 US-08-957-425-12	Sequence 14, Appl1
28	139	11.5	1822	8 US-08-822-186-1	Sequence 12, Appl1
29	139	11.5	1822	8 US-08-937-755-1	Sequence 1, Appl1
30	139	11.5	1822	8 US-08-937-755-1	Sequence 1, Appl1
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35	139	11.5	1822	10 US-09-039-107-1	Sequence 1, Appl1
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41	139	11.5	1822	14 US-10-050-050-16	Sequence 16, Appl1
42	139	11.5	1878	10 US-09-954-456-1824	Sequence 1824, Appl1
43	139	11.5	1878	12 US-10-286-152A-7	Sequence 7, Appl1
44	139	11.5	1878	12 US-10-301-822-9	Sequence 9, Appl1
45	139	11.5	1878	12 US-10-301-822-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-08-981-490B-2
; Sequence 2, Application US/08981490B
; Publication No. US20020045568A1
; GENERAL INFORMATION:
; APPLICANT: Hottel, Jens
; APPLICANT: Pohl, Jens
; APPLICANT: Bechtold, Rolf
; APPLICANT: Paulista, Michael
; APPLICANT: Unsicker, Klaus
; TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF T
; FILE REFERENCE: 100564-07032
; CURRENT APPLICATION NUMBER: US/08/981,490B
; CURRENT FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DE/195 25 416.3
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (640)..(2142)
; OTHER INFORMATION:
US-08-981-490B-2

Query Match 100.0%; Score 1207; DB 8; Length 2703;
Best Local Similarity 100.0%; Pred. No. 5.1e-299;
Matches 1207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ACCGGCGCCCTGAACCCAGGACGACACCCCTCCCAACAGGAGGCTACAGCCG 60
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OY	661	GGCGGTGAGACCTCCGTGGGCTGTGGCTTCGACCGCGCGCCCGGCAAGTCCACAGAAAGC	720
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Db      2139  CAGGTAG 2145

RESULT 2
US-09-945-182-3
; Sequence 3, Application US/09945182
; Patent No. US20020160494A1
; GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
          Mozney, John
          Rosen, Vicki A.
          Wolfman, Neil A.
          Thomson, Gerald H.
          Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSER: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,324
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lazari, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: MP52
FEATURE:
NAME/KEY: CDS
LOCATION: 845..1204
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-945-182-3

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Best Local Similarity 99.9%; Pied. No. 1.2e-288;
Matches 1206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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us-09-901-556c-1.rnpb

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Db      1464 CAGTCGGAAGGACCTGCACTGCACTCAAGGACATGGGCTGGGAGCTGGATATGCG 1523
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Db      1584 CCGTGAAGCCACGATTCATGATGATCAGACCCCTGATGATGATGATGATGATGATGATG 1643
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Db      1644 CACACACCCACCTGCTGTGCTGCGCAGCGGCTGAGTCCCATCAGATCTCTTCAATTGA 1703
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Db      1704 CTCTGCCAAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1763
Oy      1201 CAGGTAG 1207
Db      1764 CAGGTAG 1770

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RESULT 5
US-09-880-708-9

; Sequence 9, Application US/09880708
; Patent No. US2002015361A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin

; Huiyin, Thanh

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego

```

STATE: CA
COUNTRY: USA
ZIP: 92121-2189
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,708
FILING DATE: 12-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/145,060
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Halle, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 619/677-1465
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2329 base pairs
TYPE: nucleic acid
STRANDNESS: single
MOLECULE TYPE: Genomic DNA
IMMEDIATE SOURCE:
CLONE: GD-5
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 322..1806
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-880-708-9

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Query Match 86.1%; Score 1039; DB 10; Length 2329;

Best Local Similarity 91.3%; Pred No. 4.5e-256;

Matches 1102; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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Db      663 GACTGTGACCCCAAAAGGAGAGCTTCTGGGGCAAGCATCTTCAAAAGGAGATCTGC 722
Oy      121 CCCGAGCTCTCTGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
Db      723 CCCGAGCTCTCTGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
Oy      181 GCGGTTGCGCCACCCCATCACACCCAGAGTACATGCTCTGCTGTACAGAGAGCT 240
Db      783 GCGGTTGCGCCGCGCCCATCACACCCAGAGTACATGCTCTGCTGTACAGAGAGCT 842
Oy      241 GTCCGATGCTGACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Db      843 GTCCGATGCTGACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 902
Oy      301 CACCATACACACCTTATTTGACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db      903 CACCATACACACCTTATTTGACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 962
Oy      361 GAGGTAGCTGTTTGAATAGTGCCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Db      963 GAGGTAGCTGTTTGAATAGTGCCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1022
Oy      421 GATCTTGGGGAAGAGCCCTGCGAGACGCGCAAGCAGCGGCGCCCGAGGCGGGCG 480
Db      1023 GATCTTACGGAAGAGCCCTTGGAGCTGCGCAAGCAGCGGCGCCAGTAGCGGGCGG 1082

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481 TCCGACGTTGAAGCTGTCCAGCTGGCCGAGCGGCGGCGGCGGCTCTCTGATGAT 540
1083 TCCCACTGGAAGCTGTCCAGCTGGCCGAGCGGCGGCGGCGGCGGCTCTCTGATGAT 1142
541 GCGCTCCGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
1143 GCGCTCCGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1202
601 CCGAAACTTTAAGAACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
1203 CCGAAACTTTAAGAACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1262
661 GCGCGTGAACCTCCGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
1263 GCGCGTGAACCTCCGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1322
721 CCGTTCCTGCTGT 780
1323 CCGTTCCTGCTGT 1382
781 CCGTTCCTGCTGT 840
1383 CCGTTCCTGCTGT 1442
841 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
1443 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1502
901 CAGTGGGAAGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
1503 CAGTGGGAAGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1562
961 ACCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
1563 ACCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1622
1021 CCGTGGAGGCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
1623 CCGTGGAGGCGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1682
1081 CACACACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
1683 CACACACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1742
1141 CCGTGGCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1200
1743 CCGTGGCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1802
1201 CAGGTAG 1207
1803 CAGGTAG 1809

RESULT 6

US-08-945-459A-4
Sequence 4, Application US/08945459A

Publication No. US2002010263A1

GENERAL INFORMATION:

APPLICANT: MARISHIMA, FUSAO; TAKAMATSU,
APPLICANT: HIROYUKI, MIKI; HIDEO, KAMAI,
APPLICANT: SHINJI, KIMURA, MICHIO, MATSUMOTO,
APPLICANT: TOMOKI, KATSUURA, MIERO, ENOMOTO,
APPLICANT: KOICHI, SATOH, YUSUKE
TITLE OF INVENTION: A NOVEL PROTEIN AND
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: PROCESS FOR PREPARING THE SAME
ADDRESS: BIERMAN, MUSERLIAN AND LUCAS
ADDRESS: LLP
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK

FILE REFERENCE: 146.1286

COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: IBM PC COMPATIBLE
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,459A
FILING DATE: 09-DEC-1997
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: PCT/JP96/01062
FILING DATE: 19-APR-1996
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: JP7/322403
FILING DATE: 17-NOV-1995
APPLICATION DATA:
APPLICATION NUMBER: JP7/93664
FILING DATE: 19-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: UNKNOWN

US-08-945-459A-4

Query Match 29.4%; Score 355.4; DB 8; Length 357;
Best Local Similarity 99.7%; Pred. No. 2.2e-81;
Matches 356; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

848 CCACTGGCCACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 907
1 CCACTGGCCACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
908 AAGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 967
61 AAGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
968 GAGTACGAGGCTTCCAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1027
121 GAGTACGAGGCTTCCAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
1028 CCCAGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1087
181 CCCAGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
1088 CCCAGCTGGCTGT 1147
241 CCCAGCTGGCTGT 300
1148 AACAACTGGT 1204
301 AACAACTGGT 357

RESULT 7

US-09-068-253-1
Sequence 1, Application US/09068253

Patent No. US20020168381A1

GENERAL INFORMATION:

APPLICANT: SHIMURA, Takesada
APPLICANT: TORIYAMA, Satsuki
TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
FILE REFERENCE: 146.1286

Thu Aug 28 08:27:32 2003

us-09-901-556c-1.rnpb

Page 8

[illegible]

RESULT 9
US-09-94

Sequence 25, Application US/09945182
Patent No. US20020160494A1
GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.

Wozney, John
Rosen, Vicki A.
Wolfman, Neil

Thomsen, Gerald H.
Melton, Douglas A.

```

: TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
:
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
:

```

ADDRESSEE: GENETICS INSTITUTE, INC
STREET: 87 Cambridgepark Drive
CITY: Cambridge

STATE: Massachusetts
COUNTRY: USA
FID: 00140

ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 1.0

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; POLYMER: POLYMER ACCORD #1.0, VERSION #1.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/945,182
; FILING DATE: 21 May 2001

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FILING DATE: 31-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 PUBLICATION NUMBER: 2001

APPLICATION NUMBER: 08/808,324
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

```

; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 52

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851

```

; INFORMATION FOR SEQ ID NO: 25:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 1171 base pairs

```

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Human HT-1 proto

```

1         CEONE, human vE-1 protein
2         ;
3         ;
4         FEATURE:
5         NAME/KEY: CDS
6         LOCATION: 2..254

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; LOCATION: 2..964
;
; FEATURE:
; NAME/KEY: mat_peptide
;

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;          LOCATION: 605..964
;          SEQUENCE DESCRIPTION: SEQ ID NO: 25
US-09-945-182-25

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Query Match	20.88;	Score 251.6;	DB 10;	Length 1171,
Best Local Similarity	79.18;	Pred. No. 8,4e-55;		

Matches 299; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

590 CGCCGGCGGCGCAGGCGCTTGGCAGTGGCAGCGGCACGGCAGAGATGCC 649

QY	AAGCGTCGTCGACGTGAGAACATGCAATGTCACATTAAGAACATGGCTGGAGACAC	949
Db	650 AAGGCTACGCTGCAGCAAGAACGCCCTGCAGGTCAACTTCAAGACACTGGCTGGAGACAC	709
QY	950 TGGATCATCCACACCCCTTATGATGACGAGGCTTTCACATGCGAGAGGGCTGTGGATTCCCA	1009
Db	710 TGGATTATCCCGCCCTGTGAGTACGAGGCCATTCACATGCGAGGCGTGTATGGACTTCCCG	769
QY	1010 TTGGGCTCCCACTGAGGCCACGAATATGACATGTCACACCCATGATGAATCTCAAG	1065
Db	770 CTGGCTGCTGCACCTGGAGCCACCAACACAGCCATCATCCAGACGCTGATGAATCTCAAG	829
QY	1070 GACCCCGAGTGCACACACACCGTCGCTGTGTGTCGCCACGCGGCTGATGTCCTACACATC	1125
Db	830 GACCCCGGCTGCACCCCGGCCACGCTGCTGGCTGCCACCAATTTACCTCCCATACATTT	889
QY	1130 CTCTTCAATATACATCTGCACAAAGCTGTGTATTAACACTATAGACAGATGTCGTCGAG	1185
Db	890 CTATACATCAACCGCGGCATATATGTGTCTACACAGAGTACGAGGACATGTGTGTGAG	949
QY	1190 TCGTGTGGCTGCAGGTAG 1207	
Db	950 TGTGTGGCTGCAGGTAG 967	

RESULT 1
US-09-73

Sequence 12, Application US/09730772
Patent No. US2001001131A1
GENERAL INFORMATION.

APPLICANT: Luyten
APPLICANT: MOOS,
APPLICANT: Obs

APPLICANT: CHANG, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: PROTEINS

```

; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbé, Martens, Olson & Bear

```

STREET: 620 New
CITY: Newport
STATE: CA

```

;      COUNTRY: U.S.A.
;      ZIP: 92660
;      COMPUTER READABLE FORM
;

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-; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatibl
; OPERATING SYSTEM: Wind

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; SOFTWARE: FastSEQ for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: HS/09/730.772
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1  AUTORIZATION NUMBER: 05/03/1981/112
2  FILING DATE:
3  CLASSIFICATION:
4  PRIOR APPLICATION DATA:

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PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/836,081
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,

REFERENCE/DOCKET NUMBER: NH099.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEO ID NO:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1308 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA

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MOBILE 1
US-09-730-772-12

Query Match	20.18; Score 242.8; DB 9; Length 1308;
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Best Local Similarity 79.0%; Pred. No. 1.5e-52;
Matches 289; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY CGGGGGGGCCACATGCGCATCGCCAGGCGAAGGCCAGCAAGACCTTAAGGCTGCG 898
DB 943 CGGGGGACGGCTTCGCCAGCCGCCAGGCGCAAGCGCGCAAGATCGAGGCTGCGC 1002
QY 899 TGCAGTCGAAGGAGGAGCTGATGTCATCTCAAGGAGCATGGGCTGGAGAGCTGATCATC 958
DB 1003 TGCAGCAAGAGAGCCCTTCAGCTGATGATCAAGGAGCTGGGCTGGAGAGCTGATCATC 1062
QY 959 GCACCCCTTGAGTACGAGGCTTTCCACTGCGAGGGGCTGCTGAGATCCATTCGCTCC 1018
DB 1063 GCGGCCCTGAGTACGAGGCTTACCATCGAGGGGCTGCTGAGATCCCTTACGCTCG 1122
QY 1019 CACCTGAGGAGGAGGATGATGATCATCTCCAGAGGCTGATGATCATGATGATGATGATG 1078
DB 1123 CACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1182
QY 1079 TGCACACACACACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1138
DB 1183 TGCACACACACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1242
QY 1139 GACTCTGCCAACAAGCTGTGTATAGCAGTATGAGCAGATGCTGCTGCTGCTGCTGCTG 1198
DB 1243 GACGCGGGCAATATGTGTCTACAAAGATGAGAGGAGATGTGTGTGTGTGTGTGTGTG 1302
QY 1199 TGCAGG 1204
DB 1303 TGCAGG 1308

RESULT 11

US-09-735-849-12

; Sequence 12, Application US/09735849

; Patent No. US20010037017A1

; GENERAL INFORMATION:

; APPLICANT: Luyten, Frank P.

; APPLICANT: Moos, Jr., Malcolm

; APPLICANT: Chang, Steven Chao-Huan

; TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive, 16th Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/735,849

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/836,081

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bartfield, Neil S

; REGISTRATION NUMBER: 39,901

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-235-8550

; TELEFAX: 619-235-0176

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1308 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-735-849-12

Query Match 20.1%; Score 242.8; DB 9; Length 1308;

Best Local Similarity 79.0%; Pred. No. 1.5e-52;

Matches 289; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY CGGGGGGGCCACATGCGCATCGCCAGGCGAAGGCCAGCAAGACCTTAAGGCTGCG 898
DB 943 CGGGGGACGGCTTCGCCAGCCGCCAGGCGCAAGCGCGCAAGATCGAGGCTGCGC 1002
QY 899 TGCAGTCGAAGGAGGAGCTGATGTCATCTCAAGGAGCATGGGCTGGAGAGCTGATCATC 958
DB 1003 TGCAGCAAGAGAGCCCTTCAGCTGATGATCAAGGAGCTGGGCTGGAGAGCTGATCATC 1062
QY 959 GCACCCCTTGAGTACGAGGCTTTCCACTGCGAGGGGCTGCTGAGATCCATTCGCTCC 1018
DB 1063 GCGGCCCTGAGTACGAGGCTTACCATCGAGGGGCTGCTGAGATCCCTTACGCTCG 1122
QY 1079 TGCACACACACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1138
DB 1183 TGCACACACACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1242
QY 1139 GACTCTGCCAACAAGCTGTGTATAGCAGTATGAGCAGATGCTGCTGCTGCTGCTGCTG 1198
DB 1243 GACGCGGGCAATATGTGTCTACAAAGATGAGAGGAGATGTGTGTGTGTGTGTGTGTG 1302
QY 1199 TGCAGG 1204
DB 1303 TGCAGG 1308

RESULT 12

US-09-945-182-31

; Sequence 31, Application US/09945182

; Patent No. US20020160494A1

; GENERAL INFORMATION:

; APPLICANT: Celeste, Anthony J.

; APPLICANT: Mooney, John

; APPLICANT: Rosen, Vicki A.

; APPLICANT: Wolman, Neil

; APPLICANT: Melton, Douglas A.

; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENETICS INSTITUTE, INC.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/945,182

; FILING DATE: 31-Aug-2001

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/808,324

; FILING DATE: <unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Lazar, Steven R.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2003, 10:18:31 ; Search time 83 Seconds

(without alignments)
766.860 Million cell updates/sec

Title: US-09-901-556c-3

Perfect score: 2133
Sequence: 1 PEGPEPKRCHPPQTRQATAR.....ANNVYKQEDMVESCCGR 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
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- 25: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2133	100.0	401	AA040800	TGF-beta-like clone
2	2133	100.0	501	AA069600	New TGF-beta fam1
3	2133	100.0	501	AA036100	Human MP52. Homo
4	2133	100.0	501	AA019210	Human TGF-beta pro
5	2133	100.0	501	AA011900	Human high mol. wt
6	2133	100.0	501	AA001799	Human MP52 protein
7	2133	100.0	501	AA012770	Human bone morphog
8	2133	100.0	501	AA044868	TGF-beta superfam1
9	2133	100.0	501	AA033008	Human MP52. Homo

10	2122	99.5	501	22	AA070529	Human TGF-beta MP5
11	2094	98.2	501	17	AA095635	Cartilage-derived
12	2094	98.2	501	21	AA092034	Human growth diffe
13	1996	93.6	495	15	AA060022	Growth differentia
14	1996	93.6	495	22	AA084550	Amino acid sequenc
15	1996	93.6	495	24	AA076018	Mouse growth diffe
16	986	46.2	193	22	AA022940	Novel human enzyme
17	917.5	43.0	455	22	AA050216	Human growth/diffe
18	917.5	43.0	455	23	AA079173	Human growth/diffe
19	917.5	43.0	455	23	AA017604	Human extracellular
20	903	42.3	436	17	AA095636	Cartilage-derived
21	771	36.1	321	16	AA078730	Human mature VL-1
22	771	36.1	321	18	AA026591	Human bone morphog
23	771	36.1	321	22	AA010982	Human full length
24	771	36.1	321	22	AA073298	Human bone morphog
25	752.5	35.3	450	24	AA037118	NOVX protein seque
26	752.5	35.3	450	24	AA057347	Human secreted pro
27	660	30.9	263	16	AA078739	Murine mW2 protein
28	660	30.9	263	18	AA026595	Murine BMP-13 homo
29	658	30.8	120	16	AA078731	Murine protein MP5
30	658	30.8	120	18	AA026590	Human MP52 protein
31	658	30.8	120	22	AA010973	Human MP-52 protei
32	658	30.8	120	24	AA073290	Amino acid sequenc
33	658	30.8	388	16	AA078734	Human bone morphog
34	658	30.8	388	18	AA026592	Human bone morphog
35	658	30.8	388	22	AA010986	Human bone morphog
36	658	30.8	388	24	AA073302	Human bone morphog
37	655	30.7	263	22	AA010985	Murine partial mW2
38	655	30.7	263	24	AA073301	Amino acid sequenc
39	654	30.7	119	17	AA006920	Human MP52 growth
40	654	30.7	119	18	AA019846	Human bone inducin
41	652	30.6	120	23	AA051932	Human TGFbeta prot
42	648	30.4	119	21	AA070752	Wild type mature h
43	648	30.4	119	21	AA070756	Methionine oxidase
44	648	30.4	119	21	AA070757	Methionine alkylat
45	648	30.4	119	21	AA070758	Tryptophan allylat

ALIGNMENTS

RESULT 1	AA040800	standard; Protein; 401 AA.
ID	AA040800	
NC	AA040800	
XX		
XX	25-MAR-2003	(updated)
DT	11-FEB-1994	(first entry)
DT		
XX		
DE	TGF-beta-like clone MP-52 protein.	
XX		
KW	Human; transforming growth factor; beta; TGF-beta; pharmaceutical;	
KW	bone; cartilage; tooth; wound repair; immunosuppressor;	
KW	organ transplant; cosmetic surgery; antibody; diagnosis.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9316099-A2.	
PD	19-AUG-1993.	
XX		
PF	12-FEB-1993;	93WO-EP00350.
XX		
XX	12-FEB-1992;	92EP-0102324.
PR		
PA	(BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.	
XX		
PI	Hoelten G, Neidhardt H;	
XX		
DR	WPI: 1993-272824/34.	
DR	N-PSDB: AA047709.	
XX		

PT New transforming growth factor-beta family proteins and DNA -
 PT used in tissue and wound repair, in treatment of bone, cartilage
 PT and tooth defects, and antibodies for diagnosis

PS Claim 11; Page 19; 29pp; English.

XX The sequences given in AAR40800 and AAR45447 represent fragments of
 CC embryo and liver derived human transforming growth factor-beta
 CC (TGF-beta) respectively. The full length protein may be used in a
 CC pharmaceutical composition for the treatment of various bone, cartilage
 CC or tooth defects and in tissue and wound repair processes. These
 CC proteins may also be used as immunosuppressors in organ transplants and
 CC in cosmetic surgery. Antibodies raised against these proteins may be
 CC used for diagnostic purposes.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 401 AA;

Query Match 100.0%; Score 2133; DB 14; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2,7e-182;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PGPEPRKGPOTROATARTVTPKGLPGKAPKAGSVPSFLLTKARREGPREPKE 60
 DB 1 PGPEPRKGPOTROATARTVTPKGLPGKAPKAGSVPSFLLTKARREGPREPKE 60
 OY 61 PPRPPPTTPHEMYLSYRTLSADNRKGNSSVKLEAGLANITTSFDKGDGRGVYRKQ 120
 DB 61 PPRPPPTTPHEMYLSYRTLSADNRKGNSSVKLEAGLANITTSFDKGDGRGVYRKQ 120
 OY 121 RYVFDISALEKDGELGAEIRLTKRKPSDTAKPAAPGGGAAQIKLSSCPGROPASLIDV 180
 DB 121 RYVFDISALEKDGELGAEIRLTKRKPSDTAKPAAPGGGAAQIKLSSCPGROPASLIDV 180
 OY 181 RSVPGLDGSGWEVDIMKLFERNFNSAQLCLELEAMERGRAVDLRLGIDRAAROVHKA 240
 DB 181 RSVPGLDGSGWEVDIMKLFERNFNSAQLCLELEAMERGRAVDLRLGIDRAAROVHKA 240
 OY 241 LFLVFGRTKKRDLEFNEIKARSGODDKTYEYLFESORRRRAPLATROGKRPSKILKARC 300
 DB 241 LFLVFGRTKKRDLEFNEIKARSGODDKTYEYLFESORRRRAPLATROGKRPSKILKARC 300
 OY 301 SRKALHVNFKDMGMDMIAPLEYEAFHCEGLCEPFLRSHTLEPTNHAIVQTLMSNDPES 360
 DB 301 SRKALHVNFKDMGMDMIAPLEYEAFHCEGLCEPFLRSHTLEPTNHAIVQTLMSNDPES 360
 OY 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCR 401
 DB 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCR 401

RESULT 2

AAR69600 standard; Protein: 501 AA.

XX AAR69600:

DT 25-MAR-2003 (updated)
 DT 10-OCT-1995 (first entry)

DE New TGF-beta family member - MP-52 protein sequence.

KV Transforming growth factor-beta family; mitogenic; differentiation;
 KV treatment; prevention; disease; bone; cartilage; connective tissue;
 KV skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
 KV tissue regeneration; arthritis; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH 382
 FT Peptide /label= mature protein
 XX

PN W09504819-A1.

XX 16-FEB-1995.

XX 09-AUG-1994; 94AO-BP02630.

XX 10-AUG-1993; 93DE-4326829.

XX 25-MAY-1994; 94DE-4418222.

XX 09-JUN-1994; 94DE-4420157.

XX (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.

XX Hotten G, Neidhardt H, Paulista M, Hoelten G;

XX WPI; 1995-090897/12.

XX N-PSDB; AA083695.

XX New DNA encoding a new member of the TGF beta family - and
 PT related vectors, host cells etc., has mitogenic and
 PT differentiation inducing activity, e.g. for treating or
 PT preventing diseases of bone and cartilage etc.

XX Claim 6; Page 36; 51pp; German.

XX The amino acid sequence of a novel member of the transforming growth
 CC factor-beta (TGF-beta) family named MP-52. The gene encodes a protein
 CC of 501 amino acids (Aa). The protein, or at least the mature protein,
 CC has mitogenic and/or differentiation inducing properties useful in
 CC the treatment or prevention of diseases of bone, cartilage, connective
 CC tissue, skin, mucosa, epithelium or dental tissue. The protein can also
 CC be used for wound healing and tissue regeneration e.g. in osteoporosis
 CC and arthritis.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 501 AA;

Query Match 100.0%; Score 2133; DB 16; Length 501;
 Best Local Similarity 100.0%; Pred. No. 3,7e-182;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PGPEPRKGPOTROATARTVTPKGLPGKAPKAGSVPSFLLTKARREGPREPKE 60
 DB 101 PGPEPRKGPOTROATARTVTPKGLPGKAPKAGSVPSFLLTKARREGPREPKE 160
 OY 61 PPRPPPTTPHEMYLSYRTLSADNRKGNSSVKLEAGLANITTSFDKGDGRGVYRKQ 120
 DB 61 PPRPPPTTPHEMYLSYRTLSADNRKGNSSVKLEAGLANITTSFDKGDGRGVYRKQ 220
 OY 121 RYVFDISALEKDGELGAEIRLTKRKPSDTAKPAAPGGGAAQIKLSSCPGROPASLIDV 180
 DB 221 RYVFDISALEKDGELGAEIRLTKRKPSDTAKPAAPGGGAAQIKLSSCPGROPASLIDV 280
 OY 181 RSVPGLDGSGWEVDIMKLFERNFNSAQLCLELEAMERGRAVDLRLGIDRAAROVHKA 240
 DB 281 RSVPGLDGSGWEVDIMKLFERNFNSAQLCLELEAMERGRAVDLRLGIDRAAROVHKA 340
 OY 241 LFLVFGRTKKRDLEFNEIKARSGODDKTYEYLFESORRRRAPLATROGKRPSKILKARC 300
 DB 341 LFLVFGRTKKRDLEFNEIKARSGODDKTYEYLFESORRRRAPLATROGKRPSKILKARC 400
 OY 301 SRKALHVNFKDMGMDMIAPLEYEAFHCEGLCEPFLRSHTLEPTNHAIVQTLMSNDPES 360
 DB 401 SRKALHVNFKDMGMDMIAPLEYEAFHCEGLCEPFLRSHTLEPTNHAIVQTLMSNDPES 460
 OY 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCR 401
 DB 461 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCR 501

RESULT 3

AAW36100 standard; Protein: 501 AA.

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Page 4

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Db      281  |||
OY      241  |||
Db      341  |||
OY      301  |||
Db      401  |||
OY      361  |||
Db      461  |||

RESULT 5
ID      AAM1900 standard; Protein; 501 AA.
XX      AAM1900;
XX      28-OCT-1997 (first entry)
DE      Human high mol. wt. protein MP52, a growth/differentiation factor.
KW      Growth factor; differentiation; bone induction; osteoporosis; teeth;
KW      tooth; dental; joint tissue; mucous membrane; skin; nails;
KW      wound healing; regeneration; skeletal disorder; fracture; dimer.
OS      Homo sapiens.
XX      W09704095-A1.
XX      06-FEB-1997.
XX      24-JUL-1996; 96MO-JP02065.
XX      24-JUL-1995; 95JP-0218022.
XX      (FARH ) HOECHST JAPAN LTD.
XX      (FARH ) HOECHST PHARM & CHEM KK.
XX      Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
XX      WPI; 1997-132636/12.
XX      N-PSDB; AAT61412.
XX      High molecular weight human MP52 growth or differentiation factor -
XX      promotes bone induction, is useful for treatment and prevention of
XX      bone disease
XX      Claim 1; Page 12-16; 25pp; Japanese.
XX      AAM1900 is a high mol. wt. form of a human growth/differentiation
XX      factor MP52. MP52 promotes bone induction and is useful for plastic
XX      reconstruction surgery, cosmetic facial treatment, bone transplantation
XX      and prevention of disorders of bone formation, bone transplantation
XX      tissue skin, mucous membranes, nails or teeth; cartilage, joint
XX      fracture; and for the treatment of skeletal disorders and
XX      Sequence 501 AA.

Query Match
Best Local Similarity 100.0%; Score 2133; DB 18; Length 501;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1  FGGPEPKGHPOTKATATVTPKGLDGGKAPKAGVSSFLKKAREGPREKE 60
OY  1  FGGPEPKGHPOTKATATVTPKGLDGGKAPKAGVSSFLKKAREGPREKE 60
Db  101  FGGPEPKGHPOTKATATVTPKGLDGGKAPKAGVSSFLKKAREGPREKE 60
XX  101  FGGPEPKGHPOTKATATVTPKGLDGGKAPKAGVSSFLKKAREGPREKE 60
XX  160  FGGPEPKGHPOTKATATVTPKGLDGGKAPKAGVSSFLKKAREGPREKE 160
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OY      61  |||
Db      161  |||
OY      121  |||
Db      221  |||
OY      181  |||
Db      281  |||
OY      241  |||
Db      341  |||
OY      301  |||
Db      401  |||
OY      361  |||
Db      461  |||

RESULT 6
ID      AAM01799 standard; Protein; 501 AA.
XX      AAM01799;
XX      15-OCT-1997 (first entry)
DE      Human MP52 protein.
KW      Human; MP52; transforming growth factor; TGF; beta; medication;
KW      treatment; prevention; nervous system; disease; neuropathology;
KW      aging.
XX      Homo sapiens.
XX      DE19525416-A1.
XX      16-JAN-1997.
XX      12-JUL-1995; 95DE-1025416.
XX      12-JUL-1995; 95DE-1025416.
XX      (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX      Bechtold R, Hoelten G, Paulista M, Pohl J, Unsicker K;
XX      WPI; 1997-079343/08.
XX      N-PSDB; AAT59405.
XX      Medicaments contg. protein MP52 - useful for treating neurological
XX      disorders
XX      Claim 2; Pages 12-14; 21pp; German.
XX      The present sequence is the human MP52 protein, which is
XX      described in WO 9316099 and 9504819 as a member of the human
XX      transforming growth factor beta superfamily. Active MP52 can be
XX      used in a medicament to treat and prevent nervous system diseases,
XX      and/or to treat neuropathological conditions caused by nervous
XX      system ageing.
XX      Sequence 501 AA.

Query Match
Best Local Similarity 100.0%; Score 2133; DB 18; Length 501;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1  FRRPPTTPEHYMLSTYRLSPADRRKGNSSVLEKGLANTITSPIDKODRGRPVYRK 120
OY  161  FRRPPTTPEHYMLSTYRLSPADRRKGNSSVLEKGLANTITSPIDKODRGRPVYRK 120
Db  121  RYFDISALEKGLGALRTIKRPSDIAPKAPGGAOKLSSCPGROPASILDY 180
OY  221  RYFDISALEKGLGALRTIKRPSDIAPKAPGGAOKLSSCPGROPASILDY 180
Db  181  RYFDISALEKGLGALRTIKRPSDIAPKAPGGAOKLSSCPGROPASILDY 180
OY  281  RSVPGDLSGWEVDFDIWKLFNFKNSAOLCLELWAMERGRAVDLRLGDFDRAKQVHEKA 240
Db  241  LFLVFGRTKRDLEFNEIKARSGODDKTYEYLFSSORRRRAPLATROGKRPSTNLKARC 300
OY  341  LFLVFGRTKRDLEFNEIKARSGODDKTYEYLFSSORRRRAPLATROGKRPSTNLKARC 300
Db  301  SRKALHVNFKDMGMDWTIAPLEEAFHCEGCEPILSHLEPTNNAVITOTLNSMDPS 360
OY  401  SRKALHVNFKDMGMDWTIAPLEEAFHCEGCEPILSHLEPTNNAVITOTLNSMDPS 360
Db  361  TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 401
OY  461  TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 401
Db  461  TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 401
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QY 1 PGPEPRKPGHPQTRQATARTVTPKQOLPGKAPRAGSVPSFLLKKAREPGPREPKE 60
DB 101 PGPEPRKPGHPQTRQATARTVTPKQOLPGKAPRAGSVPSFLLKKAREPGPREPKE 160
QY 61 PRPPPTTPHEHYMLSLYRTLSDADRRKGNSSVYLEGLANTTTSFIDKGODDRGPVVRKQ 120
DB 161 PRPPPTTPHEHYMLSLYRTLSDADRRKGNSSVYLEGLANTTTSFIDKGODDRGPVVRKQ 220
QY 121 RYVFDISALEKDGILGAELRLIRKKRSPDAKPAAPGGGAAOLKLSGSGRQPSLLDY 180
DB 221 RYVFDISALEKDGILGAELRLIRKKRSPDAKPAAPGGGAAOLKLSGSGRQPSLLDY 280
QY 181 RSVPGIDSGGWEVFDIWKLFERNFKNSAQLCLELEAMERGRAVDLRLGDFDRAAROVHEKA 240
DB 281 RSVPGIDSGGWEVFDIWKLFERNFKNSAQLCLELEAMERGRAVDLRLGDFDRAAROVHEKA 340
QY 241 LFLVGRTRTKRDLFENEIRKARSGODDKTYEYLFSGRRRRAPLARTROGKRPSKILKARC 300
DB 341 LFLVGRTRTKRDLFENEIRKARSGODDKTYEYLFSGRRRRAPLARTROGKRPSKILKARC 400
QY 301 SRKALHVNFKDMGMDMIITAPLEYEAFHCEGLCEPFLRSHLPTNHAVIQTLMNSMDPS 360
DB 401 SRKALHVNFKDMGMDMIITAPLEYEAFHCEGLCEPFLRSHLPTNHAVIQTLMNSMDPS 460
QY 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCCR 401
DB 461 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCCR 501

RESULT 7
AAW12770
ID AAW12770 standard; protein; 501 AA.
AC AAW12770;
XX
XX 11-MAY-1997 (first entry)
DT
XX
XX Human bone morphogenic factor MP52 Arg.
DE
XX Bone morphogenic factor; MP52 Arg; bone; cartilage; skin;
KW connective tissue; mucous membrane; epithellium; teeth;
KW wound healing; vulnery; tissue regeneration; osteoporosis;
KW bone fracture; dental implant; osteoblast.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Peptide 1..27
XX Cleavage-site /label= Sig_peptide
XX /note= "sequencing suggests MP52 Arg is processed
XX /note= "proteolytically at Arg380-Arg381"
XX Cleavage-site 381..382
XX /note= "alternative cleavage site at Arg381-ALA382"
XX Mat-protein 381..501
XX /label= Mat-protein
XX /note= "mature MP52 Arg preferred for use in
XX compsns. of the invention"
XX
XX W09706254-A1.
XX
XX 20-FEB-1997.
XX
XX 02-AUG-1996; 96WO-EP03427.
XX
XX 03-AUG-1995; 95EP-0112241.
XX
XX (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.
XX Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
XX PI
XX WPI; 1997-154261/14.

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DR N-PSDB; AAT59729.
XX
XX New human bone morphogenic factor, MP52 Arg - used in the treatment
PT of osteoporosis and bone fracture, and for promoting bone regrowth
XX
XX Claim 1; Page 12-15; 26pp; English.
PS
XX
XX Novel human bone morphogenic factor MP52 Arg (AAW12770) is a growth
CC factor that induces formation of cartilage from undifferentiated
CC mesenchymal cells and which stimulates the differentiation and
CC maturation of osteoblasts. It is effective for treating/preventing
CC bone diseases caused by abnormal bone metabolism such as
CC osteoporosis. It also accelerates the healing of bone fractures,
CC and is useful for orthopaedic reconstruction, bone transplantation,
CC and dental therapeutics because of its bone morphogenetic activity.
CC It is also effective for preventing/treating cartilage, skin,
CC connective tissue, mucous membrane, teeth and epithelial disorders.
CC Recombinant MP52 Arg can be produced in host (e.g. CHO) cells
CC utilizing an isolated DNA sequence (AAT59729) in plasmid pMS599.
XX
XX Sequence 501 AA:
SQ
Query Match 100.0%; Score 2133; DB 18; Length 501;
Best Local Similarity 100.0%; Pred. No. 3.7e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PGPEPRKPGHPQTRQATARTVTPKQOLPGKAPRAGSVPSFLLKKAREPGPREPKE 60
DB 101 PGPEPRKPGHPQTRQATARTVTPKQOLPGKAPRAGSVPSFLLKKAREPGPREPKE 160
QY 61 PRPPPTTPHEHYMLSLYRTLSDADRRKGNSSVYLEGLANTTTSFIDKGODDRGPVVRKQ 120
DB 161 PRPPPTTPHEHYMLSLYRTLSDADRRKGNSSVYLEGLANTTTSFIDKGODDRGPVVRKQ 220
QY 121 RYVFDISALEKDGILGAELRLIRKKRSPDAKPAAPGGGAAOLKLSGSGRQPSLLDY 180
DB 221 RYVFDISALEKDGILGAELRLIRKKRSPDAKPAAPGGGAAOLKLSGSGRQPSLLDY 280
QY 181 RSVPGIDSGGWEVFDIWKLFERNFKNSAQLCLELEAMERGRAVDLRLGDFDRAAROVHEKA 240
DB 281 RSVPGIDSGGWEVFDIWKLFERNFKNSAQLCLELEAMERGRAVDLRLGDFDRAAROVHEKA 340
QY 241 LFLVGRTRTKRDLFENEIRKARSGODDKTYEYLFSGRRRRAPLARTROGKRPSKILKARC 300
DB 341 LFLVGRTRTKRDLFENEIRKARSGODDKTYEYLFSGRRRRAPLARTROGKRPSKILKARC 400
QY 301 SRKALHVNFKDMGMDMIITAPLEYEAFHCEGLCEPFLRSHLPTNHAVIQTLMNSMDPS 360
DB 401 SRKALHVNFKDMGMDMIITAPLEYEAFHCEGLCEPFLRSHLPTNHAVIQTLMNSMDPS 460
QY 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCCR 401
DB 461 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCCR 501

RESULT 8
AAW44868
ID AAW44868 standard; protein; 501 AA.
AC AAW44868;
XX
XX 24-SEP-1998 (first entry)
DT
XX
XX TGF-beta superfamily subunit.
DE
XX
XX TGF-beta; calcium phosphate matrix; bioactive implant; parodontosis;
KW bone replacement; cartilage; bone; fracture.
XX
XX Synthetic.
XX
XX DE19647853-A1.
XX
XX 20-MAY-1998.

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Page 6

XX	19-NOV-1996;	96DE-1047853.
PF		
XX		
PR	19-NOV-1996;	96DE-1047853.
XX		
PA	(BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.	
PA	(GERO-) GERONTOCARE GMBH BIOMATERIALS & MEDICAL.	
XX		
XI	Helde H, Pabst J, Paulista M, Pohl J;	
XX		
XX	WPI: 1998-287890/26.	
PT		
PT	Bioactive implant material for bone replacement - comprising	
XX	ostogenic calcium phosphate matrix coated with protein	
PS	Claim 3; Page 8-10; 12pp; German.	
XX		
XX		
CC	The TGF-beta superfamily subunit can be used together with a calcium	
CC	phosphate matrix to produce a bioactive implant material for bone	
CC	replacement. The implant has cartilage and/or bone-forming activity and	
CC	can be used for local treatment of cartilage and/or bone diseases or	
CC	damage caused by trauma, surgery, degeneration or reloading. The	
CC	implant can also be used for the treatment of bone defects, e.g.	
CC	parodontosis or fractures and in cosmetic and plastic surgery for fixing	
XX	mobile bones.	
XX		
XX		
Sequence	501 AA;	

[illegible]

XX	Homo sapiens.	
OS	Key	Location/Qualifiers
FH	Peptide	1-27
FT	Peptide	/label= sig-peptide
ET	Peptide	28-501
XX		/label= mat-peptide
FN	MO9743408-A1.	
XX		
PI	20-NOV-1997.	
DR	13-MAY-1997;	97WO-JP01603.
XX	07-MAY-1997;	97JP-0131631.
PR	13-MAY-1996;	96JP-0141137.
XX	(FARH) HOECHST PHARM & CHEM KK.	
PA	Jitsukawa T., Kitagawa H., Nakagawa H., Yanagisawa S;	
XX	WPI: 1998-008877/01.	
DR	.NP-PDB; AKR88340.	
XX		
PT	Mouse anti-human MP52 monoclonal antibody - recognises the dimeric	
PT	form of MP52, i.e. not the monomer, and does not cross-react with	
XX	TGF-beta or BMP-2	
PS	Disclosure; Pages 31-35; 46pp; Japanese.	
XX		
CC	The present sequence, human MP52, was used in the	
CC	preparation of a novel mouse monoclonal antibody (Mab) which	
CC	recognises dimeric but not monomeric human MP52. The Mab has a	
CC	heavy chain of subclass gamma, and does not cross-react with	
CC	TGF-beta or BMP-2. The Mab may be used to purify and assay human	
CC	MP52, especially recombinant MP52.	
XX		
SO	Sequence 501 AA;	
	Query Match	
	Best Local Similarity 100.0%; Score 2133; DB 19; Length 501;	
	Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 PGCPERRPGHPROTROATARTVPKQLPGKAPKACSVSSFLTKKAREPPPREPE	60
Db	101 PGCEPKREHPQTRQATARTVPEKQGLPGKAPKACSVSSFLTKKAREPPPREPE	160
OY	61 PPPRPPIIPHEMLSLYRTLSADRKGRGSSVKLEAGLANTITTSIFDKGDGRGVVRKO	120
Db	161 PPPRPPIIPHEMLSLYRTLSADRKGRGSSVKLEAGLANTITTSIFDKGDGRGVVRKO	220
OY	121 RYVPISALKEODLIGAEILRLKKRPSDPAPAPGGGRAOLKLSCSGSGROPASILDY	180
Db	221 RYVEDISALKEDGLGAELIRLLKKRPSDPAFAFGGGRRAOLKLSCSGSGROPASILDY	240
OY	181 RSVVGDLGSWEVEFDWKLFNFKNNSAOLCIELEAMERGRAVDLGCDFDAARQVHEKA	280
Db	281 RSVVGDLGSWEVEFDWKLFNRNNSAOLCIELEAMERGRAVDLGCDFDAARQVHEKA	340
OY	241 LTFVSGTRKRRIEAFNEIKARGSGDDTVTYEYLFSORRRRAPPLATRGRRPSKINAKC	300
Db	341 LTFVSGTRKRRIEAFNEIKARGSGDDTVTYEYLFSORRRRAPPLATRGRRPSKINAKC	360
OY	301 SRKALHVNKDGMDNDTIAPLEYAFHCEGLCEEPULSHLEPNNAVIOTLNMSMDYES	400
Db	401 SRKALHVNFCKMGDDWTIAPLEYAFHCEGLCEEPULSHLEPNNAVIOTLNMSMDYES	460
OY	361 TPPTCCVPTRLSPISILFIDSANNVYYQEDNVESCGCR 401	
Db	461 TPPTCCVPTRLSPISILFIDSANNVYYQEDNVESCGCR 501	

RESULT 10
AAB70529 standard; Protein; 501 AA.
ID AAB70529 standard; Protein; 501 AA.
XX AAB70529;
AC AAB70529;
XX 08-MAY-2001 (first entry)
DE Human TGF-beta MP52 protein sequence SEQ ID NO.2.
XX
XX Human; transforming growth factor-beta; monomeric protein; MP52;
KW MP13; dimeric protein; TGF-beta; vulnary; antitumor; neutrotic;
KW neutrotic; antitumor; osteopathic; gene therapy; bone;
KW cartilage; dental; wound healing; connective tissue.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 465 /note="unspecified"
FT
XX
XX EPI074620-A1.
XX
XX 07-FEB-2001.
XX
XX 06-AUG-1999; 99EP-0115613.
XX
XX 06-AUG-1999; 99EP-0115613.
XX
XX (HYGE-) HYGE AG C/O MAEDER & BAUMGARTNER TREUH.
XX
XX WPI; 2001-228100/24.
XX
XX N-PSDB; AAF74420.
XX
XX
XX Novel monomeric protein of transforming growth factor-beta family for
PT prevention or therapy of diseases associated with bone; cartilage
PT damage; promotion of wound healing, has substitution or deletion of
PT cysteine -
XX
XX
XX Claim 8; Page 14-16; 31pp; English.
XX
XX The present invention describes a protein (I) selected from the members
CC of the transforming growth factor-beta (TGF-beta) superfamily, which is
CC monomeric due to substitution or deletion of a cysteine which is
CC responsible for dimer formation. Also described are: (I) nucleic acid
CC (II) encoding (I); (2) expression vector (III) containing (II) in a
CC suitable vector system; (3) host cell (IV) containing (III) capable of
CC producing (I); and (4) a pharmaceutical composition (V) containing (I),
CC (II), (III) or (IV). (I) has vulnary, antitumor, neutrotic,
CC neutrotic, antitumor, and osteopathic activities, and can be
CC used in gene therapy. (V) is useful for the prevention or therapy of
CC diseases for which also the dimeric form of the protein would be
CC indicated. Diseases treatable include diseases associated with bone
CC and/or cartilage damage or affecting bone and/or cartilage disease or
CC situations in which cartilage and/or bone growth is desirable, for spinal
CC fusion, for damaged or diseased tissue associated with connective tissue
CC including tendon and/or ligament, periodontal or dental tissue including
CC dental implants, neural tissue including CNS tissue and neuropathological
CC situations, tissue of the sensory system, liver, pancreas, cardiac,
CC blood vessel, renal, uterine and thyroid tissue, skin, mucous membrane,
CC endothelium, epithelium, for promotion or induction of nerve growth,
CC tissue regeneration, angiogenesis, wound healing including ulcers, burns,
CC injuries or skin grafts, induction of proliferation of progenitor cells
CC or bone marrow cells, for maintenance of a state of proliferation or
CC differentiation, for treatment or preservation of tissue or cells for
CC organ or tissue transplantation, for integrity of gastrointestinal lining
CC and for treatment of disturbances in fertility, contraception or
CC pregnancy. The present sequence represents the specifically claimed
CC TGF-beta monomeric protein MP52, from the present invention.
XX
XX Sequence 501 AA.

Query Match 99.5%; Score 2122; DB 22; Length 501;

Best Local Similarity 99.8%; Pred. No. 3.5e-181;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PGGPEPKGHPQOTQATRTVTYPPGOLPGKAPKAGVSSFLTKRAREGPPPEKE 60
DB 101 PGGPEPKGHPQOTQATRTVTYPPGOLPGKAPKAGVSSFLTKRAREGPPPEKE 160
QY 61 PFRPPITPHEMYLSTYRTLSADRRGKSSVYKLEGLANTITTSIDKGDGRGVYVKKQ 120
DB 161 PFRPPITPHEMYLSTYRTLSADRRGKSSVYKLEGLANTITTSIDKGDGRGVYVKKQ 220
QY 121 RYVFDISALEKDGILGAELRIIRKKPSTAKPAAPGGGAAQKLSSCPGROPASLDY 180
DB 221 RYVFDISALEKDGILGAELRIIRKKPSTAKPAAPGGGAAQKLSSCPGROPASLDY 280
QY 181 RSVPGDGSQGVFPIWIKFRNPKNSAOICLLEMERGRAVDLGLGFDRAAROVHEKA 240
DB 281 RSVPGDGSQGVFPIWIKFRNPKNSAOICLLEMERGRAVDLGLGFDRAAROVHEKA 340
QY 241 LFLVFGRTKKRDLFNEIKARSGODKTYEYELFSQRRRRAPLATROGRKPSKILKARC 300
DB 341 LFLVFGRTKKRDLFNEIKARSGODKTYEYELFSQRRRRAPLATROGRKPSKILKARC 400
QY 301 SRKALHVNFKDGMDDWITAPLEYEAFHCEGLCEPPLRSHPETHNAVYQTLMSMDPES 360
DB 401 SRKALHVNFKDGMDDWITAPLEYEAFHCEGLCEPPLRSHPETHNAVYQTLMSMDPES 460
QY 361 TPPTCCVPTRLSPISILFTDSANNVYKQEDMVESGCCR 401
DB 461 TPPTCCVPTRLSPISILFTDSANNVYKQEDMVESGCCR 501

RESULT 11
AAR95635 standard; Protein; 501 AA.
ID AAR95635 standard; Protein; 501 AA.
XX AAR95635;
XX
XX 25-OCT-1996 (first entry)
XX
XX
XX Cartilage-derived morphogenetic protein-1.
XX
XX
XX Human; cartilage-derived morphogenetic protein-1; CDMP-1;
KW articular cartilage; chondrogenic; vulnary; implantation;
KW chondromalacia; osteoarthritis; therapy; joint repair.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Peptide 2..19 /note="Signal peptide"
FT
FT Region 2..377 /note="Pro-region"
FT
FT Modified-site 189..191 /note="N-glycosylation site"
FT
FT Cleavage-site 378..381 /note="Proteolytic processing site"
FT
FT Domain 382..501 /note="Mature C-terminal domain"
FT
FT Peptide 388..400 /note="Antigen (AAR95642) used to raise antibodies"
FT
FT Peptide 417..447 /note="Highly conserved consensus motif (AAR95641)"
XX
XX WO9614335-A1.
XX
XX 17-MAY-1996.
XX
XX 07-NOV-1994; 94WO-US12814.
XX
XX 07-NOV-1994; 94WO-US12814.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

QY 61 PRRPPTTPHEXMSLYRTLSADRRKGNSSVYKLEAGLANTITSTFDKGGDDRGPPVVRKQ 120
 DB 161 PRRPPTTPHEXMSLYRTLSADRRKGNSSVYKLEAGLANTITSTFDKGGDDRGPPVVRKQ 220
 QY 121 RYVEPISALEKDGILGAEIRLIRKRPSTAKPAAGGGRAOLKSSCPGSPALDVR 180
 DB 221 RYVEPISALEKDGILGAEIRLIRKRPSTAKPAAGGGRAOLKSSCPGSPALDVR 280
 QY 181 RSVPLDSSGWEVDFIMKLFNFKNASQCLLEAMERGAVDLGLGFDRAARQVHEKA 240
 DB 281 RSVPLDSSGWEVDFIMKLFNFKNASQCLLEAMERGAVDLGLGFDRAARQVHEKA 340
 QY 241 LFLVFGRTKRDLEFNEIKANSQDDKTYVEYLFSSQRRKRAAPLAFQGRPSKNLAKAR 300
 DB 341 LFLVFGRTKRDLEFNEIKANSQDDKTYVEYLFSSQRRKRAAPLAFQGRPSKNLAKAR 400
 QY 301 SRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPLSHLEPTNHAVIQTLMNSMDPE 360
 DB 401 SRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPLSHLEPTNHAVIQTLMNSMDPE 460
 QY 361 PPTCCVPTRLSPISILFIDSANNNVYKQYEDMVESGCR 401
 DB 461 PPTCCVPTRLSPISILFIDSANNNVYKQYEDMVESGCR 501

RESULT 13

AAR60022
 ID AAR60022 standard; Protein; 495 AA.

AAR60022;

25-MAR-2003 (updated)
 15-MAR-1995 (first entry)

Growth differentiation factor 5.

DE GDF-5; growth differentiation factor 5; diagnostic; therapeutic;
 XX GDF-5; growth differentiation factor 5; diagnostic; therapeutic;
 KW detection; treatment; cell proliferative disorders; uterus tissue;
 KM skeletal tissue; uterine acoplasm; endometriosis; reagent;
 XX suppression; transforming growth factor beta superfamily; TGF beta.

Mus musculus.

Key Location/Qualifiers

Modified-site 183

/note="potential glycosylation site"

Cleavage-site 371..375

/note="putative tetrabasic proteolytic processing site"

Cleavage-site 384..385

/note="putative tetrabasic proteolytic processing site"

W09415949-A1.

21-JUL-1994.

12-JAN-1994; 94MO-US000657.

12-JAN-1993; 93US-0003144.

(UYUO) UNIT JOHNS HOPKINS SCHOOL MED.

Huyun T, Lee S;

WPI. 1994-249127/30.

N-PSDB; AA070010.

New growth differentiation factor-5 - used to develop prods. for
 the detection or treatment of cell proliferative disorders of the
 uterus or skeletal tissue

PS Claim 1; Fig 1; 79pp; English.

XX AAR60022 shows the amino acid sequence of Growth differentiation
 CC factor 5, which is encoded by AA070010. The GDF-5 sequence contains
 CC a core of hydrophobic amino acids near the N-terminus, suggestive
 CC of signal sequence secretion. The sequence contains all of the
 CC highly conserved residues present in other members of the
 CC transforming growth factor beta superfamily, including the seven
 CC cysteine residues with their characteristic spacing. The prods. of the
 CC invention can be used for detection of a cell proliferative disorder
 CC of the uterus or skeletal tissue which is associated with GDF-5
 CC expression. Antisense sequences of GDF-5 can be used to treat uterine
 CC neoplasm, endometriosis, or skeletal disorders (claimed). The prods.
 CC can also be used in eg. contraception, in vitro fertilisation or in
 CC preventing premature labour.
 CC (updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 495 AA;

Query Match 93.6%; Score 1996; DB 15; Length 495;

Best Local Similarity 94.5%; Pred. No. 6, 6e-170;

Matches 378; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

QY 2 GSEPRKPGHPOTATARTVTPKQQLPGKAPPAAGVPSFLLKAREPPEPPEP 61
 DB 96 GSEPRKPGHPOTATARTVTPKQQLPGKAPPAAGVPSFLLKAREPPEPPEP 155

QY 62 PRRPPTTPHEXMSLYRTLSADRRKGNSSVYKLEAGLANTITSTFDKGGDDRGPPVVRKQ 121
 DB 156 PRRPPTTPHEXMSLYRTLSADRRKGNSSVYKLEAGLANTITSTFDKGGDDRGPPVVRKQ 215

QY 122 YVEPISALEKDGILGAEIRLIRKRPSTAKPAAGGGRAOLKSSCPGSPALDVR 181
 DB 216 YVEPISALEKDGILGAEIRLIRKRPSTAKPAAGGGRAOLKSSCPGSPALDVR 275

QY 182 SVPGIDSGWEVDFIMKLFNFKNASQCLLEAMERGAVDLGLGFDRAARQVHEKA 241
 DB 276 SVPGIDSGWEVDFIMKLFNFKNASQCLLEAMERGAVDLGLGFDRAARQVHEKA 335

QY 242 FLVFGRTKRDLEFNEIKANSQDDKTYVEYLFSSQRRKRAAPLAFQGRPSKNLAKAR 301
 DB 336 FLVFGRTKRDLEFNEIKANSQDDKTYVEYLFSSQRRKRAAPLAFQGRPSKNLAKAR 395

QY 302 SRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPLSHLEPTNHAVIQTLMNSMDPE 361
 DB 396 SRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPLSHLEPTNHAVIQTLMNSMDPE 455

QY 362 PPTCCVPTRLSPISILFIDSANNNVYKQYEDMVESGCR 401
 DB 456 PPTCCVPTRLSPISILFIDSANNNVYKQYEDMVESGCR 495

RESULT 14

AAB84550

ID AAB84550 standard; Protein; 495 AA.

AAB84550;

05-SEP-2001 (first entry)

Amino acid sequence of growth differentiation factor-5 (GDF-5).

Growth differentiation factor-5; GDF-5; transforming growth factor beta;

TGF-beta; uterine tissue; skeletal tissue; contraception; fertility;

pregnancy; cell proliferative disease; uterine neoplasm; endometriosis;

prenatal screening; cartilage differentiation; skeletal development.

Unidentified.

Key Location/Qualifiers

Modified-site 183

/note="potential N-glycosylation site"

Region 371..375

FT /note="tetraplastic proteolytic processing site"
 FP 384..385
 PT /note="tetraplastic proteolytic processing site"
 PN US6245896-B1.
 XX 12-JUN-2001.
 XX 01-SEP-1998: 9805-0145060.
 XX 31-MAY-1995: 9505-0455559.
 PR 12-JAN-1993: 9305-0003144.
 PR 12-JAN-1994: 94WO-US000657.
 XX (UJJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PA Lee S. Huynh T;
 PI WPI: 2001-424329/45.
 DR N-PSDB: AAH28140.
 XX New antibodies that bind growth differentiation factor-5, useful for in
 PT vivo or in vitro immunodiagnosis or immunotherapy, particularly for
 PT detecting or treating a cell proliferative disorder of the uterus or
 PT skeletal system
 PS Claim 1; Fig 2A-B; 34pp; English.
 XX
 CC The present sequence represents growth differentiation factor-5 (GDF-5).
 CC GDF-5 is a member of the transforming growth factor beta (TGF-beta)
 CC superfamily. Unlike other members of the TGF-beta family, the expression
 CC of GDF-5 is highly tissue specific, being expressed in cells primarily
 CC in uterine tissue and skeletal tissue. GDF-5 polypeptides and
 CC polynucleotides may be used for contraception, fertility, pregnancy and
 CC cell proliferative diseases. They may be used for detecting neoplasms
 CC of uterine origin, and also for the detection of diseases such as
 CC endometriosis. In addition, GDF-5 may also be useful as an indicator of
 CC developmental anomalies in prenatal screening procedures. As GDF-5
 CC is expressed in early embryogenesis, it may be used to treat cell
 CC proliferation, cartilage differentiation diseases and skeletal
 CC development diseases.
 CC
 CC Sequence 495 AA:
 SO
 Query Match 93.6%; Score 1996; DB 22; Length 495;
 Best local similarity 94.5%; Pred. No. 6.6e-170;
 Matches 378; Conservative 2; Mismatches 20; Indels 0; Gaps 0;
 OY 2 GGPERKPGHPOTRATARTYTPKRGOLPGKAPPKAGSVSSFLTKARPPRPKRP 61
 DB 96 GGSERKPGSPSOTRKAARTYTPKRGOLPGKASKASABSSFLTKRTPKPGPRPKRP 155
 OY 62 FRPPPTTPEHYMLSTYRFLSDADKGNSSVKLEAGLANTTTFIDKGGDDRRPVYRKR 121
 DB 156 FRPPPTTPEHYMLSTYRFLSDADKGNSSVKLEAGLANTTTFIDKGGDDRRPVYRKR 215
 OY 122 YFIDISALEKDBLGAELRLIRKRPSTANPAAPGGGAAQLKSSCPGROPASILDYR 181
 DB 216 YFIDISALEKDBLGAELRLIRKRPSTANPAAPGGGAAQLKSSCPGROPASILDYR 275
 OY 182 SVPGIDSGMEVFIDWLKFRNFKNSAOLCLELEMERGRAVDRLGDFPRAAROVHEKAL 241
 DB 276 SVPGIDSGMEVFIDWLKFRNFKNSAOLCLELEMERGRAVDRLGDFPRAAROVHEKAL 335
 OY 242 ELYVGRTRKRLDFREITAKRSGODKTVYELYSQRRKRAPLATOGRRPSKNTAKRCS 301
 DB 336 ELYVGRTRKRLDFREITAKRSGODKTVYELYSQRRKRAPLATOGRRPSKNTAKRCS 395
 OY 302 RKAHAVNEFKMGMDWIIAPLEYEAFHCCEGLCEFPPLRSHLEPTNNAVITOTLANSMDPEST 361
 DB 396 RKAHAVNEFKMGMDWIIAPLEYEAFHCCEGLCEFPPLRSHLEPTNNAVITOTLANSMDPEST 455
 OY 362 PPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCR 401

DB 456 PPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCR 495
 RESULT 15
 ID ABG76018
 ID ABG76018 standard; Protein; 495 AA.
 AC ABG76018;
 DE 30-APR-2003 (first entry)
 DE Mouse growth differentiation factor-5, GDF-5.
 XX
 KW GDF-5; growth differentiation factor 5; TGF-beta; mouse;
 KW transforming growth factor beta; skeletal development; endometriosis;
 KW cartilage differentiation; cell proliferative disease; uterine tumour;
 KW bone dysplasia; spondylophyseal dysplasia; achondroplasia;
 KW dysplasia epiphysealis; metaphyseal dysostosis; hyperchondroplasia;
 KW enchondromatosis; hypophosphatasia; osteopetrosis; hyperphosphatasia;
 KW craniofacial dysplasia; osteogenesis imperfecta; transgenic;
 KW idiopathic osteoporosis; Engelmann's disease.
 XX
 OS Mus sp.
 PN US2002165361-A1.
 PD 07-NOV-2002.
 XX 12-JUN-2001; 2001US-0880708.
 PF 31-MAY-1995: 9505-0455559.
 PR 01-SEP-1998: 9805-0145060.
 PR 12-JAN-1993: 9305-0003144.
 PR 12-JAN-1994: 94WO-US000657.
 XX (LEES/) LEE S.
 PA (HUYNH/) HUYNH T.
 PI Lee S. Huynh T;
 XX WPI: 2003-246676/25.
 DR N-PSDB: ABX11590.
 XX
 PT New antibody specifically binding to a GDF-5 polypeptide, useful for
 PT diagnosing and treating cell proliferative disorders with aberrant
 PT GDF-5 activity, such as endometriosis, uterine tumors and those
 PT involving skeletal tissues
 PS Claim 1; Fig 2; 36pp; English.
 XX
 CC The invention relates to an antibody that specifically binds to growth
 CC differentiation factor-5 (GDF-5, a member of the TGF-beta (transforming
 CC growth factor beta) superfamily of proteins) polypeptide appearing
 CC as ABG76018. In order to determine the biological activity of GDF-5 in
 CC vivo, transgenic mice were constructed that express GDF-5 ectopically.
 CC Analysis of two independent transgenic mouse lines showed that these
 CC animals have ectopic bone formation with evident muscle tissue. This
 CC showed that GDF-5 was capable of inducing bone formation in vivo.
 CC The antibody is useful for the diagnosis and treatment of cell
 CC proliferative disorders associated with aberrant GDF-5 activity, such
 CC as endometriosis, cartilage tumors, those involving skeletal tissues,
 CC endometriosis, uterine tumors, those involving skeletal tissues,
 CC uterine tumour, bone dysplasia, spondylophyseal dysplasia,
 CC achondroplasia, dysplasia epiphysealis, metaphyseal dysostosis,
 CC hyperchondroplasia, enchondromatosis, hypophosphatasia, osteopetrosis,
 CC idiopathic osteoporosis and Engelmann's disease. The present sequence
 CC represents mouse GDF-5.
 XX
 SO Sequence 495 AA:
 Query Match 93.6%; Score 1996; DB 24; Length 495;

Best Local Similarity 94.5%; Pred. No. 6.6e-170;
Matches 378; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy	2	GGEPRKPHAPOTROTATATVYPKOLPGKAPRPAAGSVSSFLTKKAEPGPREPKKE	61
Db	96	GGSEKPPSSSOTROAAARTVTPKQOLPEGKASKAGSAPSSFLTKTKEPGPREPKE	155
Qy	62	FRPPITPEHYMLSLYRTLSDADRRGKSSVLALEGLANTITSFDKGODDRGPVVRKOR	121
Db	156	FRPPITPEHYMLSLYRTLSDADRRGKSSVLALEGLANTITSFDKGODDRGPVVRKOR	215
Qy	122	YVFEDISALEKOGLLCAELRLTKKRSSTDAKPAAPGGGAAOITKLSSCPGSGROPASTLDYR	181
Db	216	YVFEDISALEKOGLLCAELRLTKKRLPDVAKPAVPSSGGRVAOLKLTSSCPGSGROPASTLDYR	275
Qy	182	SVPGIDSGWGEVFDLWKLFPRNFKNNSAOCLLEAEMRGRAVDLRIGLGFERTAROVHEKAL	241
Db	276	SVPGIDSGWGEVFDLWKLFPRNFKNNSAOCLLEAEMRGRAVDLRIGLGFERTAROVHEKAL	335
Qy	242	FLVEGRTKKRDLFENEIKARSGODDKRYEYLFESORRRRAPLATROGKRPSKNLAKRS	301
Db	336	FLVEGRTKKRDLFENEIKARSGODDKRYEYLFESQRRKRRAPLANOGRKPSKNLAKRS	395
Qy	302	RKALHVNKKDKGMDWMTIAPLEYEAFHCEGICEPFLRSILFPTNNAVIOTLANSMDPEST	361
Db	396	RKALHVNKKDKGMDWMTIAPLEYEAFHCEGICEPFLRSILFPTNNAVIOTLANSMDPEST	455
Qy	362	PPTCGVPTRLSPISILFIDSANNNVYKOEEDWVVEGCGR	401
Db	456	PPTCGVPTRLSPISILFIDSANNNVYKOEEDWVVEGCGR	495

Search completed: August 19, 2003, 10:28:14
Job time : 85 secs

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Db 461 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 2

A55452
 C:Species: Homo sapiens (man)
 C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-2000
 C:Accession: A55452
 J:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak
 A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth
 A:Reference number: A55452; MUID:95050604; PMID:7961761
 A:Accession: A55452
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-501 <CHA>
 A:Cross-references: GB:013660; NID:9600731; PID:9600732
 A:Gene: GDB:CDMP1
 A:Cross-references: GDB:438940
 C:Superfamily: Inhibin

Query Match
 Best Local Similarity 98.2%; Score 2094; DB 2; Length 501;
 Matches 394; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PGGEPRGHPOTROTATATVPKQOLPGKAPPAAGSVSSFLTKAREGPPREPE 60.
 Db 101 PGGEPRGHPOTROTATATVPKQOLPGKAPPAAGSVSSFLTKAREGPPREPE 160
 QY 61 PFPPPTTPEHYMLSTYRLSDADRGKSSVYLEAGLANITTSFDKGGDDRGVAVKQ 120
 Db 161 PFPPPTTPEHYMLSTYRLSDADRGKSSVYLEAGLANITTSFDKGGDDRGVAVKQ 220
 QY 121 RYFEDISALEKDLGAEILIRKRPSPAKPAAGCGRAOLKSSCPGROPASLLDV 180
 Db 221 RYFEDISALEKDLGAEILIRKRPSPAKPAAGCGRAOLKSSCPGROPASLLDV 280
 QY 181 RSVPGIDSGWEVFDIMKLFNFKNSAOLCLELAWERGRAVDLGLGFDRAARQVHEKA 240
 Db 281 RSVPGIDSGWEVFDIMKLFNFKNSAOLCLELAWERGRAVDLGLGFDRAARQVHEKA 340
 QY 241 LFLVGRTRKRDLEFNEIKARSGODDKVYELYSQRRKRAPLATROGKRPSKNLKARC 300
 Db 341 LFLVGRTRKRDLEFNEIKARSGODDKVYELYSQRRKRAPLATROGKRPSKNLKARC 400
 QY 301 SRKALHVFNKMGMDWIIAPLEYEAFHCEGLCEPLRSHEPTNNAVIOTLANSMDPES 360
 Db 401 SRKALHVFNKMGMDWIIAPLEYEAFHCEGLCEPLRSHEPTNNAVIOTLANSMDPES 460
 QY 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 401
 Db 461 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 3

S43294
 Done morphogenetic protein-related protein (GDP5) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
 C:Accession: S43294
 R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
 A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
 A:Reference number: S43294; MUID:94195427; PMID:8145850
 A:Accession: S43294
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-495 <STO>
 A:Cross-references: GB:008337; NID:9488461; PID:AAA18778.1; PID:9488462
 C:Superfamily: Inhibin

Query Match
 Best Local Similarity 93.6%; Score 1996; DB 2; Length 495;
 Matches 378; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 GGEPRGHPOTROTATATVPKQOLPGKAPPAAGSVSSFLTKAREGPPREPE 61
 Db 96 GGEPRGHPOTROTATATVPKQOLPGKAPPAAGSVSSFLTKAREGPPREPE 155
 QY 62 PFPPPTTPEHYMLSTYRLSDADRGKSSVYLEAGLANITTSFDKGGDDRGVAVKQ 121
 Db 156 PFPPPTTPEHYMLSTYRLSDADRGKSSVYLEAGLANITTSFDKGGDDRGVAVKQ 215
 QY 122 YFEDISALEKDLGAEILIRKRPSPAKPAAGCGRAOLKSSCPGROPASLLDV 181
 Db 216 YFEDISALEKDLGAEILIRKRPSPAKPAAGCGRAOLKSSCPGROPASLLDV 275
 QY 182 SVPGIDSGWEVFDIMKLFNFKNSAOLCLELAWERGRAVDLGLGFDRAARQVHEKA 241
 Db 276 SVPGIDSGWEVFDIMKLFNFKNSAOLCLELAWERGRAVDLGLGFDRAARQVHEKA 335
 QY 242 FLVGRTRKRDLEFNEIKARSGODDKVYELYSQRRKRAPLATROGKRPSKNLKARC 301
 Db 336 FLVGRTRKRDLEFNEIKARSGODDKVYELYSQRRKRAPLATROGKRPSKNLKARC 395
 QY 302 RKALHVFNKMGMDWIIAPLEYEAFHCEGLCEPLRSHEPTNNAVIOTLANSMDPES 361
 Db 396 RKALHVFNKMGMDWIIAPLEYEAFHCEGLCEPLRSHEPTNNAVIOTLANSMDPES 455
 QY 362 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 401
 Db 456 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 495

RESULT 4

B55452
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000
 C:Accession: B55452
 J:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak
 A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming gr
 A:Reference number: B55452; MUID:95050604; PMID:7961761
 A:Accession: B55452
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-436 <CHA>
 A:Cross-references: GB:013661; NID:9632489; PID:AAA61416.1; PID:9632490
 C:Superfamily: Inhibin

Query Match
 Best Local Similarity 42.3%; Score 903; DB 2; Length 436;
 Matches 200; Conservative 62; Mismatches 109; Indels 74; Gaps 14;

QY 7 KPGHPOTROTATATVPKQOLPGKAPPAAGSVSSFLTKAREGPPREPE 66
 Db 16 KPGHPOTROTATATVPKQOLPGKAPPAAGSVSSFLTKAREGPPREPE 66
 QY 67 ITTPEHYMLSTYRLSDADRGKSSVYLEAGLANITTSFDKGGDDRGVAVKQ 125
 Db 67 ITTPEHYMLSTYRLSDADRGKSSVYLEAGLANITTSFDKGGDDRGVAVKQ 125
 QY 126 ISAL-EDKGLGAEILIRKRPSPAKPAAGCGRAOLKSSCPGROPASLLDV 184
 Db 127 ISAL-EDKGLGAEILIRKRPSPAKPAAGCGRAOLKSSCPGROPASLLDV 184
 QY 185 GLDGS---GWEVFDIMKLFNFKNSAOLCLELAWERGRAVDLGLGFDRAARQVHEKA 241
 Db 176 GLDGS---GWEVFDIMKLFNFKNSAOLCLELAWERGRAVDLGLGFDRAARQVHEKA 241
 QY 225 RGLGPRRAARQVHEKALFLVGRTRKRDLEFNEIKARSGODDKVYELYSQRRKRAPLATROGKRPSKNLKARC 281

Db 235 RSLGGRVRRTPQERALLVFSRSQRTL-FAEMREQLQASAEVVGPGGAGSGGPPPP 293

QY 262 -----SGODDKTYEYELFSQRRRRAPLATROGKRPSKRLKARCSKRALHVNFKDGM 316

Db 294 PPPPSGTFPDAGLMSF--SPGRRRRRFAFSRGRKRSKRLCSKPLHVNFKELGMD 351

QY 317 WIALEFAHCEGCELPRLSHLEPTNHAVIQTLMNSMDPESTPTCCVPTRLSPISI 376

Db 352 WIALEFAHCEGCELPRLSHLEPTNHAVIQTLMNSMDPESTPTCCVPTRLSPISI 411

QY 377 LFIDSANNVYKQEDVMVYVSCGCR 401

Db 412 LYIDAGNNVYNEEMVYVSCGCR 436

RESULT 5

S43295
bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
M:Alternate names: growth and differentiation factor 6
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
C:Accession: S43295
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the
A:Reference number: S43294; MUID:94195427; PMID:8145850
A:Accession: S43295
A:Molecule type: DNA
A:Residues: 1-125 <STO>
A:Cross-references: EMBL:008338; NID:9488463; PIDN:AAA18779.1; PID:9488464
C:Genetics:
A:Gene: gdf6
C:Superfamily: Inhibin
P:1-5/Domain: polybasic protease recognition site #status predicted <PPR>
F:6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted <

Query Match 26.9%; Score 573; DB 2; Length 125;
Best Local Similarity 79.2%; Pred. No. 5.8e-36;
Matches 99; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 277 RRRRAPLATROGKRPSKRLKARCSKRALHVNFKDGMWIIAPLEFAHCEGCEP 336

Db 1 RRRRTAFASRGRKRSKRLCSKPLHVNFKELGMDWIIAPLEFAHCEGCEP 60

QY 337 LRSHLEPTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQEDVMV 396

Db 61 LRSHLEPTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQEDVMV 120

QY 397 SCGCR 401

Db 121 SCGCR 125

RESULT 6

S43296
bone morphogenetic protein-related protein (GDF7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C:Accession: S43296
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the
A:Reference number: S43294; MUID:94195427; PMID:8145850
A:Accession: S43296
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <STO>
A:Cross-references: GB:U08339; NID:9488465; PIDN:AAA18780.1; PID:9488466
C:Superfamily: Inhibin

Query Match 23.9%; Score 510; DB 2; Length 151;
Best Local Similarity 60.3%; Pred. No. 3.7e-31;
Matches 91; Conservative 22; Mismatches 12; Indels 26; Gaps 1;

QY 277 RRRRAPLATROGKRPS-----KNLKARCSKRALHVNFK 310

Db 1 RRRRTAFAGTRAGSGGGGGGGGGGGGGGGGGAGGHRRRRRSRKSLAVDF 60

QY 311 DMGMDWIIAPLEFAHCEGCELPRLSHLEPTNHAVIQTLMNSMDPESTPTCCVPT 370

Db 61 ELGMDWIIAPLEFAHCEGCELPRLSHLEPTNHAVIQTLMNSMDPESTPTCCVPT 120

QY 371 LSPISILFIDSANNVYKQEDVMVYVSCGCR 401

Db 121 LSPISILYIDANNVYKQEDVMVYVSCGCR 151

RESULT 7

JH0687
bone morphogenetic protein 2I precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JH0687; S16244
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in earl
A:Reference number: JH0687; MUID:92378616; PMID:1510675
A:Accession: JH0687
A:Molecule type: mRNA
A:Residues: 1-398 <NIS>
A:Cross-references: GB:X63424; NID:964585; PIDN:CAA5018.1; PID:964586
A:Experimental source: oocyte
R:Plesow, S.; Koester, M.; Knoechel, W.
Biochem. Biophys. Acta 1089, 280-282, 1991
A:Title: cDNA sequence of Xenopus laevis bone morphogenetic protein 2 (BMP-2).
A:Reference number: S16244; MUID:91274367; PMID:2054389
A:Accession: S16244
A:Molecule type: mRNA
A:Residues: 1-6, 'S', 8-15, 'V', 17-232, 'N', 234-398 <PLE>
A:Cross-references: EMBL:X55031; NID:964581; PIDN:CAA38850.1; PID:964582
C:Superfamily: Inhibin
C:Keywords: dimer; glycoprotein
F:285-398/Product: bone morphogenetic protein 2I #status predicted <MAT>
F:137-202,340/Binding site: carbohydrate (asn) (covalent) #status predicted <

Query Match 21.0%; Score 447; DB 2; Length 398;
Best Local Similarity 32.5%; Pred. No. 6.2e-26;
Matches 133; Conservative 57; Mismatches 135; Indels 84; Gaps 18;

QY 30 GGNAPKAGSVPSFLKARREPPREP---KEPRPPPTTHEYMLSYRI-LSQADR 85

Db 37 GRSSPOOSQVNLQFELRLSMFGLKRRPPGKNVYIP-----YMLDYHLHLQAA 90

QY 86 KGNSSVKLE---AGLANTITTFIDKGODRGPVVRK---ORVYFISALEKDGIL-GA 137

Db 91 DEGTSMADPMOMENASRANTVRSFHHESHEELPESHEKTIQRFNLSIPDELVTSA 150

QY 138 ELRLRKPS-----DTAKPAAPGGGAAQKLSSCPGSGP-ASILDY 180

Db 151 ELRIPEQVQEPESDSKRLINITYVPAA-----AASRGVYRLDIT 196

QY 181 RSPVIGDGSWEVFDIWKLFNFKNSAQCLELEAV-----ERGRAVDLKGCFDRAAR 234

Db 197 RLVNH-NEKWESEFDVTP-----AIAIRIAHKOPNHGVVEYTHLDND--K 239

QY 235 QVERKALFVFGTRKRDLE--FNEIKARGGODKIVYEVLFQRRRRAPLATROGKR 292

Db 240 NVPKKHVIRISRLTPPKDMPQRLPLVPSHGK---GHALKRQKRA---RKOR- 291

QY 293 SKNLKARCSKRALHVNFKDGMWIIAPLEFAHCEGCELPRLSHLEPTNHAVIQT 352

Db 292 -RLKSSCRNRPVLYVDFSDVGMWIVAPRGYAHFCHGCEPRLADHLNSTHAIQT 350

QY 353 MNSMDESTPTCCVPTRLSPISILFIDSANNVYKQEDVMVYVSCGCR 401

Db 351 VNSVN-TNIPKACVPTELSAISMLYIDENEKVLKNDVMVYVSCGCR 398

RESULT 8
S45355
bone morphogenetic protein-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 03-May-1996
C:Accession: S45355
R: Feng, J.O.; Harris, M.A.; Ghosh-Choudhury, N.; Feng, M.; Mundy, G.R.; Harris, S.E.
Biochim. Biophys. Acta 1218, 221-224, 1994
A:Title: Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2): comp
A:Reference number: S45355; MUID:94289485; PMID:8018727
A:Accession: S45355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <FEN>
C:Superfamily: Inhibin

Query Match 20.8%; Score 443.5; DB: 2; Length 394;
Best Local Similarity 32.8%; Pred. No. 1,1e-25;
Matches 131; Conservative 48; Mismatches 118; Indels 103; Gaps 19;
QY 42 SSFLTKKAREPGPREPEPRPPITPHEMLSLYTLSDADKRGKNSV-----KLE-95
DB 58 SMFGLKOR-----TPSKDVVPP-----YMDLYR-----RHSQGPAPADHRLER 100
QY 96 -AGLANTTTSF-----IDKGDDRGKPVYRKORVDFISALEKGLL-GAELRLKRPSPD 148
DB 101 AASNANTVTFHNEVAEEELPEMSGKTPAR--RFFNLSSVPSDEFLTSALDQIFRQIOH 158
QY 149 T-----AKPAAPGGGAAOLKSSCPGSPASLIDVRYVPGIDSGWEY 193
DB 159 ALGNSSFOHRINIYEIKRPA-----AANLKF---PYTR---LDTFLV-NONTISQMS 204
QY 194 FDIWKLEFRNFKNSAO-----LCLEEMERGKRAVDLGLDFDPAARQVH-----KAL 241
DB 205 FDTVPAMRWTTGHTNHGFFVVAHLEENPGVSKRHV---RISRLHDEHWSQIRL 261
QY 242 FLVFGKTRKRDLEFNEIKARSGQDDKTYEYLFSGRRKRAVLATROGKRPSPKNCAS 301
DB 262 LVYFGHDKG-----GHLHKKRKKQAKHQR-----KRLKSSCK 295
QY 302 KRALHYFKMGNDMIIAPLEYEAFHCEGLCEFPRLSHLEPTNNAVITQTLNMSDPEST 361
DB 296 RRLPYLDSVDGMNMIVAPPGYHAFYCHGCEPPLADHINSTHAIYQTLVNSVN-SKI 354
QY 362 PPTCCVPTPLSPISILFTDSANNVYKQEDMVVYVSCGCR 401
DB 355 PRACCVPELTAISMLYDENKEKYLKNYODMVVYVSCGCR 394

RESULT 9
S37073
bone morphogenetic protein 2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S37073
R: Feng, J.O.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
submitted to the EMBL data library, September 1993
A:Description: cDNA sequence of fetal rat calvarial osteoblast bone morphogenetic protein
A:Reference number: S37073
A:Accession: S37073
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <FEN>
A:Cross-references: EMBL:Z25868; NID:9397950; PIDN:CAA81088.1; PID:9397951
C:Superfamily: Inhibin

Query Match 20.7%; Score 440.5; DB: 2; Length 393;
Best Local Similarity 31.7%; Pred. No. 1.9e-25;
Matches 133; Conservative 54; Mismatches 131; Indels 101; Gaps 19;
QY 37 AGVSFSLTKKAREPGPREPEPRPP-----RPP---ITPHEWLSLY 77

DB 22 AGLPELGRKKRKFGASRPSPEDVLSFEFLRLSMFGLKORPSPKDVVPPYMDLY 81
QY 78 RTISDADKRGKNSV-----KLE--AGLANTTTSF-----IDKGDDRGKPVYRKORVYED 125
DB 82 R-----RHSQGPALAPHRLERAAARNVYLSFHEALDELSEMSGKTSR--RFFEN 133
QY 126 ISLEEDGLL-GAELRLKRPSPDAPKPAAPGGAAOLKIS-----SCPSGROPAS- 176
DB 134 LSSVPTDEFLTSALDQIFREQOEL-----GNSSFQHRINIYEIKRPAASSKFPYTR 187
QY 177 LIDVRSVPELDSGWEVDFIWKLEFRNFKNSAO-----LCLEEMERGKRAVDLDRGCFD 230
DB 188 LDTFLRYT-QNTSOMSEFVTPAVKRW--TAGHTNHGFFVVAHLEEKPGVSKRHV--- 241
QY 231 RAARQVH-----KALFLVGRKTRKRDLEFNEIKARSGQDDKTYEYLFSGRRKRA 282
DB 242 RISRLHDEHWSQVYRFLVYFGHDK-----GHLHKKRKKQA 281
QY 283 PLATGQKRPSPKNTKARSKRALHYFKMGNDMIIAPLEYEAFHCEGLCEFPRLSHLE 342
DB 282 KHKOR-----KRLKSSCKRHLVYDSVDGMNMIVAPPGYHAFYCHGCEPPLADHNL 335
QY 343 PTNHAVITQTLNMSDPESTPPTCCVPTPLSPISILFTDSANNVYKQEDMVVYVSCGCR 401
DB 336 STNHAIYQTLVNSVN-SKIPRACCVPELTAISMLYDENKEKYLKNYODMVVYVSCGCR 393

RESULT 10
BMH02
bone morphogenetic protein 2 precursor - human
N:Alternate names: bone morphogenetic protein 2a; rhBMP2
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: B37278; PC2178
R: Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, B.; Whitters, M.J.; Kriz, R.W.;
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: B37278
A:Molecule type: mRNA
A:Residues: 1-396 <MO2>
A:Cross-references: GB:M22489; NID:9179501; PIDN:AAA51834.1; PID:9179502
R: Ishida, N.; Tsujimoto, M.; Kanaya, T.; Shimamura, A.; Kodama, S.; Kat
J. Biochem. 115, 279-285, 1994
A:Title: Expression and characterization of human bone morphogenetic protein-2 in sil
A:Reference number: PC2178; MUID:94266754; PMID:8206877
A:Accession: PC2178
A:Molecule type: protein
A:Residues: 290-295, 'X', 297-304 <ISH>
A:Experimental source: cell line BOMO-15A1C
R: Kothore, S.; Hammarstone, K.M.; Danseure, S.; Porter, T.J.
Protein Sci. 4(Suppl.2), 443S, 1995
A:Title: N-terminal isoforms of recombinant human bone morphogenetic protein (rhBMP-2
A:Reference number: A56729
A:Contents: annotation
A:Note: determination of amino ends of mature forms; dimers with long form chains hav
C:Comment: This hormone is capable of inducing bone formation at ectopic morphologica
A:Gene: GDB: BMP2
A:Cross-references: GDB:125204; OMTW:112261
C:Map position: 20P12-20P12
C:Complex: homodimer, disulfide linked
C:Superfamily: Inhibin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-265/Domain: signal sequence #status predicted <PRO>
F:266-336/Product: bone morphogenetic protein 2, long form #status predicted <MATL>
F:283-336/Product: bone morphogenetic protein 2 #status predicted <MAT>
F:135,163,164,200/Binding site: carboxylate (Asn) (covalent) #status predicted
F:283/Modified site: pyrolysine carboxylate (Asn) (in mature form) #status exper
F:338/Binding site: carboxylate (Asn) (covalent) #status experimental

A:Description: SpDVR1, a member of the transforming growth factor-beta superfamily expd
 A:Reference number: S52408
 A:Accession: S52408
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1461 <PON>
 A:Cross-references: EMBL:248313; NID:9673496; PID:9673497
 C:Superfamily: inhibin

Query Match
 Best Local Similarity 20.1%; Score 428.5; DB 2; Length 461;
 Matches 129; Conservative 48; Mismatches 105; Indels 153; Gaps 17;

63 RPPPTTPEHYML-----SLXRTLSADARKGSSVYKLEAG-----97
 DB 82 RPPSLRGQONQFCAGFTMSYRTLNIDDSGHPSETEPOPGGLASNAIYNSPDSGIGS 141
 OY 98 -----LANTTS-----FIDKQDDRGCVVRKQRYVEDISAL-EKGL 134
 DB 142 VMSGTVEYNTREYQAVSQDITMSLPYHKDAIED-----TEHRRFDIGRIPOGETY 196
 OY 135 LGAEELRIKKRPSDTAKPAPAGGGRAGAKLSSCPGSPASL-IDVRSV--PGLDGS- 189
 DB 197 TSAELRYFR-----DAGQGRSLYKRIIDVLLRREGSDGSR 231
 OY 190 -----GWEVFDI-----WKLFRFKNSAQCLLEEMERGRAVDLRLG 228
 DB 232 SPVYLDSTIVAGDHGLVFDMTSATSTWRSYPCANVGLQ-----RVESLGLIN 281
 OY 229 FDRARQVHEKALFLVFGRTKRD-----LEFNEIKARSGODDKTYEYLFSPRRKRAPL 284
 DB 282 IDPTDAGV-----VGVNNEGREPVMYVF-----QRDEVIATNSHLRRNRRA-- 325
 OY 285 ATRO--GKRPSK-----NLKARSGRLAHNFEDMGDDMTIAPLEYE 325
 DB 326 ATQKQKGRKRPDNDIASRDSASSNSPDKCKRLKLFNFDLQMDQWTLAPLGYV 385
 OY 326 AFHCEGLCEPPLNSHLEPTNNAVITOLMNSMDESPPTCCVPTPLSPISITFIDSNVY 385
 DB 386 AFECQCECAFPLNGHNNATNNAIVOTLVHMSPSHVPOPCAPFTLSPIYLYIDDSNVV 445
 OY 386 VTKQYEDVYVESGCG 400
 DB 446 VLKTKYKMMVYVACGC 460

RESULT 14
 149542
 bone morphogenetic protein 5 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 C:Accession: J43542
 R:King: A.166, 112-122, 1994
 A:Title: BMP5, and the molecular, skeletal, and soft-tissue alterations in short ear mice
 A:Reference number: 149542; MUID:95046894; PMID:7958439
 A:Accession: J49542
 A:Molecule type: mRNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1452 <RKS>
 A:Cross-references: GB:J41145; NID:9755033; PIDN:AAA64612.1; PID:9755034
 A:Gene: BMP5
 C:Superfamily: inhibin

Query Match
 Best Local Similarity 19.9%; Score 425.5; DB 2; Length 452;
 Matches 117; Conservative 38; Mismatches 117; Indels 87; Gaps 15;

54 PPRPKRPPRPPPTTPEHYMLSLYRT--LSDADRKGNSSVRLKGIANTITSPIDKQGD 111
 DB 128 PPRTPPLTOSFP-----LASTLHDTNLTNDAD-----MVMSFNLVLR 164

OY 112 DRGPVVRKQRYV--FDISAL-EKDGILGAELRIILKKRPSDTAKPAPAGGGRAG--IKL 165
 DB 165 DKDFSHQRRHYKEFRFDLQIPIHGEAVTAAEFRYIKDK-----GNRPFNEHRIKI 214
 OY 166 SSCPSGRQPAS-----LLDVRSPGLDSSGWEVFDI-----WKLFRFKNSAQCLLEEMERG 213
 DB 215 STYQITKEYTNRDADFLDITRTQALD-VGLVYFDITVTSNHWYINQNQLGQLAEF 273
 OY 214 EMERGRAVDLRLGL-----FDRARQVHEKALFLVFGRTKRDLPENELKAR 261
 DB 274 ---GDRSTINVSAGLVGRHGPQSKOPPMVAFVFASEVILSRVPAASKRKNQ--NRKSN 328
 OY 262 SQDDDKTYEYELFSQRRRRRAPLATRQGRPSKMLKARCSKALHVFCKMGMDMTIAP 321
 DB 329 SHQDPS-----RMPESA---GDYNTSRQKQCKKHELYVFRDLGMQDMTIAP 372
 OY 322 LEYEFHCEGLCEPPLNSHLEPTNNAVITOLMNSMDESPPTCCVPTPLSPISITFID 381
 DB 373 EGYALFTCDGECSPFLNHNATNNAIVOTLVHLMFDPDHVKPCCAFTKINALSVLYFD 432
 OY 382 ANNVYRYKYEDVYVESGCG 400
 DB 433 SSNVILKTKYKMMVYVACGC 451

RESULT 15
 BMH04
 bone morphogenetic protein 4 precursor - human
 N:Alternate names: bone morphogenetic protein 2B
 C:Species: Homo sapiens (man)
 C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C:Accession: C37278
 R:Wooney, J.M.; Rosen, V.; Celeste, A.J.; Mitocek, L.M.; Willems, M.J.; Kriz, R.W.;
 Science 242, 1528-1534, 1998
 A:Title: Novel regulators of bone formation: molecular clones and activities.
 A:Reference number: A37278; MUID:89072750; PMID:3201241
 A:Accession: C37278
 A:Molecule type: mRNA
 A:Residues: 1-408 <MO3>
 A:Cross-references: GB:M2490; NID:9755033; PIDN:AAA51835.1; PID:9755034
 C:Gene: BMP4; BMP2B
 A:Cross-references: GDB:125205; OMIM:112262
 C:Map position: 14q22-14q23
 C:Superfamily: inhibin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-292/Domain: propeptide #status predicted <PRO>
 F:293-408/Product: bone morphogenetic protein 4 #status predicted <MAT>
 F:143,208,350,365/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match
 Best Local Similarity 19.8%; Score 423; DB 1; Length 408;
 Matches 118; Conservative 64; Mismatches 128; Indels 58; Gaps 15;

63 RPP-----ITFHEVMLSLYRTLSADARKGSSVYKLE-----AGLANTITSPIDKQGD 113
 DB 70 RPOFSKSAVIP-DVMDRLYRLQSGEEREDLHSTGLEPFRAPSRATVASFHEHETLN 128
 OY 114 GPVVRKQ---RYVDISAL-EKDGILGAELRIILKKRPSDTAKPAPAGGGRAGAKLSSCP 169
 DB 129 IPTGSENSAFETPLNLSIPDENIYSSAELRLFREO-VDQGPWMEGFTIRINITYEMKRP 187
 OY 170 S---GRQPASLIDVRSVPGLDSSGWEVFDI-----WKLFRFKNSAQCLLEEMERG 219
 DB 188 AEVVPGLILRLDTRLVNH-NVTWETFDVSPAVLRW--REKQNTYLALEVTHNQ 244
 OY 220 RAVDLRLGLDPRARQ---VHEKALFLVFGRTKRDLPENELKARSGQDKTYEYELF 274
 DB 245 RTHQGGHVRISRLDPSGNGMAQLRPLVTFCHDNG-----HALT 285
 OY 275 SQRKRRAPL-ATRQGRPSKMLKARCSKALHVFCKMGMDMTIAPLEYEAFHCEGLC 333

Db	286	RRRAKSPKHHSQARAKKNK	---CRHSLYDFSDVGMNDWIVAPPGIOAFYCHGDC	341
Qy	334	EEPLRSHLEPTNHAVIQTIANSMDPE	PTCCVPTRLSPISILFTIDSANNVYKQYEDM	393
Db	342	PEPLADHINSTNHAIQTLVNSVN	-SSIPKACCVPTELSATSMLYDEYDKVYLKNYQEM	400
Qy	394	VVESGCR	401	
Db	401	VVEGCGCR	408	

Search completed: August 19, 2003, 10:31:21
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: August 19, 2003, 10:18:50 ; Search time 24 Seconds

(without alignments)
785.738 Million cell updates/sec

Title: US-09-901-556c-3

Perfect score: 2133
Sequence: 1 PEGPEPKGHPQTRQATAR.....ANNVYKQYEDMVESGCR 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2133	100.0	501 1	GDF5_HUMAN
2	1996	93.6	495 1	GDF5_MOUSE
3	903	42.3	436 1	GDF6_BOVIN
4	573	26.9	125 1	GDF6_MOUSE
5	510	23.9	151 1	GDF7_MOUSE
6	448	21.0	398 1	BMP4_XENLA
7	443.5	20.8	394 1	BMP2_MOUSE
8	440.5	20.7	393 1	BMP2_RAT
9	440	20.6	396 1	BMP2_HUMAN
10	439	20.6	395 1	BMP2_RABIT
11	433	20.3	396 1	BMP2_DAMDA
12	433	20.3	405 1	BMP4_CHICK
13	432	20.3	398 1	BMP4_XENLA
14	428.5	20.1	461 1	DVR1_STRPU
15	425.5	19.9	409 1	BMP4_RABIT
16	425.5	19.9	452 1	BMP5_MOUSE
17	423	19.8	408 1	BMP4_HUMAN
18	422	19.8	401 1	BMP4_XENLA
19	420.5	19.7	454 1	BMP5_HUMAN
20	419	19.6	408 1	BMP4_MOUSE
21	417	19.5	408 1	BMP4_RAT
22	414	19.4	402 1	BMP8_HUMAN
23	410.5	19.2	395 1	UNIV_STRPU
24	409.5	19.2	588 1	DECA_DROME
25	408.5	19.2	593 1	DECA_DROME
26	408	19.1	408 1	BMP4_DAMDA
27	406.5	19.1	353 1	BMP2_CHICK
28	403	18.9	399 1	BMP4_MOUSE
29	401	18.8	510 1	BMP6_MOUSE
30	398	18.7	430 1	BMP7_MOUSE
31	397.5	18.6	431 1	BMP7_HUMAN
32	397.5	18.6	513 1	BMP6_HUMAN
33	393.5	18.4	621 1	DECA_DROPS

34	390.5	18.3	420 1	BMI0_MOUSE
35	381	17.9	372 1	DECA_TRICA
36	381	17.9	426 1	BMP7_XENLA
37	376.5	17.7	424 1	BMI0_HUMAN
38	374.5	17.6	427 1	DSTL_CHICK
39	370	17.3	472 1	BMP3_HUMAN
40	367	17.2	360 1	DVR1_XENLA
41	360.5	16.9	436 1	60A_DROVI
42	358	16.8	355 1	DVR1_BRARE
43	355.5	16.7	468 1	BMP3_RAT
44	351.5	16.5	429 1	GDF2_HUMAN
45	349.5	16.4	399 1	BMP8_MOUSE

ALIGNMENTS

RESULT 1
GDF5_HUMAN STANDARD; PRT; 501 AA.
ID GDF5_HUMAN
AC P43026; 096SBI;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Growth/differentiation factor 5 precursor (GDF-5) (Cartilage-derived morphogenetic protein 1) (CDMP-1).
GN GDF5 OR CDMP1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=95071375; PubMed=7980526;
RT "Cloning and expression of recombinant human growth/differentiation factor 5."
RT Biochem. Biophys. Res. Commun. 204:646-652(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas J.T., Volkovic S., Luyten F.P., Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
RT "Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development.";
RT J. Biol. Chem. 269:28227-28234(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jakosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Laylor S., Levesialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConachie L.J., Mclay K., McMurtry A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Selva H.K., Showman S., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20.",
RL Nature 414:665-671(2001).
RP 141
RN SEQUENCE FROM N.A.
RP TISSUE=Brain:
RX MEDLINE=22386257; PubMed=12477932:
RA Krausberg R.L., Fellnold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shannon C.M., Schuler G.D.,
RA Altshuler S.F., Jordan B., Buettner K.H., Schaefer C.F., Shat N.K.,
RA Hopkins R.F., Zerbe B., Moore T., Max S.T., Wang J.Y., Hsieh F.,
RA Diatchenko L., Marzinska K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schaefer T.E.,
RA Brownstein M.J., Ueda N.T.B., Ioshizuka M., Garavito R.P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Arranson R.D., Mullany S.J.,
RA Bosak S.A., Mckenzie P.O., Mckenzie K.J., Matek J.A., Guneratne P.H.,
RA Villalón D.K., Muzny D.M., Soedergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield J.S., Kirzylowski M.I., Skalska U., Smalhus D.B.,
RA Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.:
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.":
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
CC -1- SUBUNIT: Homodimer; disulfide-linked (by similarity).
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LONG BONES DURING
CC HUMAN EMBRYONIC DEVELOPMENT.
CC -1- DISEASE: DEFECTS IN GDF5 ARE A CAUSE OF ACROSTEOSIS
CC CHONDRODYSPLASIA OF THE HUNTER-THOMPSON TYPE. THIS FORM OF
CC DYSPLASIA IS CHARACTERIZED BY SHORT FOREARMS, HANDS AND FEET. THE
CC RADIUS IS CURVED AND ITS HEAD IS OFTEN DISLOCATED POSTERIORLY. THE
CC METACARPALS, METATARSALS AND PHALANXES ARE PARTICULARLY SHORT. THE
CC PHALANXES ARE ALMOST SQUARE.
CC -1- SIMILARITY: Belongs to the tcf-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X80915; CAAS5874.1; -;
DR EMBL; U13660; AAS57007.1; -;
DR EMBL; AL121586; CAAB94916.1; -;
DR EMBL; BC032495; AAB32495.1; -;
DR PIR; A55452; A55452.
DR PIR; JC2347; JC2347.
DR HSSP; P12643; 3BMP.
DR GeneW; HGNC:4220; GDF5.
DR MIM; 601146; -;
DR MIM; 201250; -;
DR MIM; 200700; -;
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0005515; F:protein binding activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007179; P:tgfbeta receptor signaling pathway; TAS.
DR InterPro; IPR001839; tGFP.
DR InterPro; IPR001111; tGFP_N.
DR Pfam; PF00018; tGF_beta; 1.
DR Pfam; PF00688; tGfp_propeptide; 1.
DR ProDom; PD000357; tGfb; 1.
DR SMART; SM00204; tGfb; 1.
DR PROSITE; PS00250; tGF_BETA_1; 1.
TW Signal; Growth factor; Cytokine; Glycoprotein; Dwarfism.

FT	SIGNAL	1	27	POTENTIAL.
FT	PROPEP	28	381	POTENTIAL.
FT	CHIN	382	501	GROWTH/DIFFERENTIATION FACTOR 5.
FT	DISUFID	400	466	BY SIMILARITY.
FT	DISUFID	429	498	BY SIMILARITY.
FT	DISUFID	433	500	BY SIMILARITY.
FT	DISUFID	455	465	INTERCHAIN (BY SIMILARITY)
FT	CARBOHYD	189	189	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CONFLICT	38	38	T -> S (IN REF. 2).
FT	CONFLICT	254	258	AGCG -> VPSRK (IN REF. 2).
FT	CONFLICT	276	276	S -> A (IN REF. 2).
FT	CONFLICT	321	321	A -> T (IN REF. 2).
FT	CONFLICT	381	381	L -> S (IN REF. 2).
SO	SEQUENCE	501 AA;	55410 MW;	37985F2D15D4F5EE CRC64;
Query Match				
Best Local Similarity		100.0%;	Score 2133;	DB 1; Length 501;
Matches 401; Conservative		0;	Mismatches 0;	Indels 0; Gaps 0
QY	1	PGGPERPGHPPTQQTQATRTVTPRGQDGGKAPPKAGSVPSFSLKKAREPBPPEPKE	60	
DB	101	PGGPERPGHPPTQQTQATRTVTPRGQDGGKAPPKAGSVPSFSLKKAREPBPPEPKE	160	
QY	61	PFPPRPITTHEYMLSLYRTLSDADRRGSSSVKLEAGLANTITSFIDKGDDDGPAVVRKQ	120	
DB	161	PFPPRPITTHEYMLSLYRTLSDADRRGSSSVKLEAGLANTITSFIDKGDDDGPAVVRKQ	220	
QY	121	RYEFDISALEKQGLGAELRIILRRKPSPTAKPAPPGGGAQQLTSSCPGPGPASTLBY	180	
DB	221	RYEFDISALEKQGLGAELRIILRRKPSPTAKPAPPGGGAQQLTSSCPGPGPASTLBY	280	
QY	181	RSVPGDGGSGMEYFDIWKLFRRFKNSAQCLELEAMEGRVYDLRGFGPRAAROVHERA	240	
DB	281	RSVPGDGGSGMEYFDIWKLFRRFKNSAQCLELEAMEGRVYDLRGFGPRAAROVHERA	340	
QY	241	LFYVPRTRKKRLPFNEIKRSGQDDKYVYLFSQRRKRAPATLQGRKRSKLNKAC	300	
DB	341	LFYVPRTRKKRLPFNEIKRSGQDDKYVYLFSQRRKRAPATLQGRKRSKLNKAC	400	
QY	301	SRKALVNRDKMDMDMTIAPLEPAFBCBGLCEPLRSHLEPNNAVIOTLNMSPDS	360	
DB	401	SRKALVNRDKMDMDMTIAPLEPAFBCBGLCEPLRSHLEPNNAVIOTLNMSPDS	460	
QY	361	TPPTCCVPTRLSPISLIFLIDSANNVNYROYEDMVESGCR	401	
DB	461	TPPTCCVPTRLSPISLIFLIDSANNVNYROYEDMVESGCR	501	
RESULT 2				
GDF5_MOUSE		STANDARD;	PRT;	495 AA.
ID	AC	AC	AC	
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Growth/differentiation factor 5 precursor (GDF-5).			
GN	GDF5 OR GDF-5 OR BP.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10900;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CD-1; TISSUE=Embryo;			
RC	MEDLINE=9415427; PubMed=815850;			
RA	Storm E.E., Huvnh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,			
RA	Lee S.-U.;			
RT	"limb alterations in brachypodism mice due to mutations in a new			
RT	member of the TGF beta superfamily."*			
RL	Nature 368:639-643(1994).			
CC	-1- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.			
CC	-1- SUBUNIT: Homodimer; disulfide-linked (by similarity).			
CC	-1- DISEASE: DEFECTS IN GDF5 ARE THE CAUSE OF BRACHYPODISM WHICH			

CC	ALTERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT SPARES THE AXIAL SKELETON.	CC
CC	-1- SIMILARITY: Belongs to the TGF-beta family.	CC
CC	-----	CC
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or-send-an-email-to-license@isb-sib.ch).	CC
CC	or send an email to license@isb-sib.ch).	CC
DR	EMBL: U08337; AAA18778.1; -	DR
DR	PIR: S43294; S43294.	DR
DR	HSSP: P12643; 3BMP.	DR
DR	MGD; MGI:95688; Gd15.	DR
DR	InterPro: IPR001839; TGFb.	DR
DR	InterPro: IPR001111; TGFb.N.	DR
DR	Pfam: PF000019; TGF-beta:1.	DR
DR	Pfam: PF00688; TGFb.propeptide; 1.	DR
DR	ProDom: PD000357; TGFb; 1.	DR
DR	SMART; SM0204; TGFb; 1.	DR
KW	PROSITE; PS00250; TGF_BETA_1; 1.	KW
FT	Signal; Growth factor; Cytokine; Glycoprotein; Polymorphism.	FT
FT	SIGNAL	FT
FT	PROPEP	FT
FT	CHAIN	FT
FT	DISULFID	FT
FT	DISULFID	FT
FT	DISULFID	FT
FT	DISULFID	FT
FT	CARBOHYD	FT
FT	VARIANT	FT
FT	SEQUENCE	FT
SO	495 AA; 5485 MW; CD0D5DE48185D2E3 CRC64;	SO
Query Match	93.6%; Score 1996; DB 1; Length 495;	
Best Local Similarity	94.5%; Pred. No.1.5e-130;	
Matches 378; Conservative	2; Mismatches 20; Indels 0; Gaps 0;	
QY	2 GPERPKRPNRPOTQATATATATVPKGGKAPPKAGSVSSFTLKAKAREGPPREKPEP	61
DB	96 GGSSTKGRPSSTQTRQAAARATVTPRGOLPGKASKAGAPSSFLKKTREPGTREPKEP	155
QY	62 FRPPPTPRHEMYLSLVFTLSDADRRKGNSSVYKLEAGLANTTTSFTIDKGDDRGPEYVRQR	121
DB	156 FRPPPTPRHEMYLSLVFTLSDADRRKGNSSVYKLEAGLANTTTSFTIDKGDDRGPEYVRQR	215
QY	122 VYRPTISALEKGLLGAEIRLTKRRPSPTAKRAAAGGGAADLKLSSCSGQPSLIDVR	181
DB	216 VYRPTISALEKGLLGAEIRLTKRRPSPTAKRAAAGGGAADLKLSSCSGQPSLIDVR	275
QY	182 SVPELDGSGWEVPIWIKLFNFKKNSAQCLELEMERGRAVDLGLGDFRARAVERKAL	241
DB	276 SVPELDGSGWEVPIWIKLFNFKKNSAQCLELEMERGRAVDLGLGDFRARAVERKAL	335
QY	242 FLVEGRTRKRRDLFENEIKARSGODKYVEYLFSQRRKRRAPLATRQGRPSKMLKACS	301
DB	336 FLVEGRTRKRRDLFENEIKARSGODKYVEYLFSQRRKRRAPLATRQGRPSKMLKACS	395
QY	302 RKAHNVFKMGMDWIITAPLEYAFKCEGLCEPPLNSHLEPTNHAIVQITLMSNDPEST	361
DB	396 RKAHNVFKMGMDWIITAPLEYAFKCEGLCEPPLNSHLEPTNHAIVQITLMSNDPEST	455
QY	362 PPTCCVPTRLSPISILFIDSANNVYVYKOYEDMAYVESCGR 401	
DB	456 PPTCCVPTRLSPISILFIDSANNVYVYKOYEDMAYVESCGR 495	
RESULT 3		
ID	GDF6_BOVIN	
AC	P55106	
STANDARD:	PRT: 436 AA.	
DT	01-Oct-1996 (Rel. 34, Created)	

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DR      01-OCT-1996 (Rel. 34, last sequence update)
DE      16-OCT-2001 (Rel. 40, last annotation update)
DE      Growth/differentiation factor 6 precursor (GDF-6) (Cartilage-derived
DE      morphogenetic protein 2) (CDMP-2) (Fragment).
OS      GDF6 OR CDMP2.
OC      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX      Bovidae; Bos.
OX      NCBI_TaxId=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Articular cartilage;
RX      MEDLINE=95050604; PubMed=7961761;
RA      Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,
RA      Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
RT      "Cartilage-derived morphogenetic proteins. New members of the
RT      transforming growth factor-beta superfamily predominantly expressed
RT      in long bones during human embryonic development.";
RL      J. Biol. Chem. 269:28227-28234(1994).
CC      -1 SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC      -1 SIMILARITY: Belongs to the TGF-beta family.
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or send an email to license@isb.slb.ch).
-----
DR      EMBL: U13661; AAA61416.1; -
DR      PIR: B55452; B53452.
DR      HSP: P18075; IBMF.
DR      InterPro: IPR002440; GF_cysknot.
DR      InterPro: IPR001839; TGFb.
DR      InterPro: IPR001111; TGFb_N.
DR      Pfam: PF00019; TGF-beta; 1.
DR      Pfam: PF00688; TGFb_propeptide; 1.
DR      PRINTS: PR00438; GFCYSKNOT.
DR      ProDom: PD000357; TGFb; 1.
DR      SMART: SM00204; TGFb; 1.
DR      SMART: PS00250; TGF_beta_1; 1.
KW      Growth factor; Cytokine; Glycoprotein.
FT      NON_TER          1
FT      PROPEP          <1 316
FT      CHAIN           317 436
FT      DISULFD         335 401
FT      DISULFD         364 433
FT      DISULFD         368 435
FT      DISULFD         400 400
FT      CARBOHYD        27 27
FT      CAROAMD         89 89
SQ      SEQUENCE       436 AA; 47873 MW; B0688E12EFBAED1D CRC64;
                                POTENTIAL.
                                GROWTH/DIFFERENTIATION FACTOR 6.
                                BY SIMILARITY.
                                BY SIMILARITY.
                                BR SIMILARITY.
                                INTERCHAIN (BY SIMILARITY).
                                N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                N-LINKED (GLCNAC. . . ) (POTENTIAL).
Query Match      42.3%; Score 903; DB 1; Length 436;
Best Local Similarity 44.9%; Pred. No. 2,9e-55;
Matches 200; Conservative 62; Mismatches 109; Indels 74; Gaps 14
QY      7 KPGHPQRQAATARIIVTPKGOLPGCKAPKAGSVPSFLTKKAREGPPEPPRRPP 66
DB      16 KEGRNP---RARRENATAIREPLDRQEPPIPOEEP-----QRRPQOPBARPPGR 66
QY      67 ITPHRYMLSLYTLDADRKGGNSVYLKEAGLANITTSFIDKGDODRGVP-VKQRYVED 125
DB      67 LVPHRYMLSTIYRTYSIAEKLGINASPFGSKSANITTSVDVGDLDSHTPLRKQYLLD 126
QY      126 ISAL-EKQGLCAELRIILKKRSQSDAKPAAPGGRAAOQLKSSCSGSGROPASILDVRSVP 184
DB      127 VSTLSDKDELVAADVRLFRQAPAAALAPPAA--APLAALRIPLVAPAAGS-----AEP 175
QY      185 GLDGSG--GWEEFDIMKLPLERFNFKNSAQCLTELE-AM-ERRGRA-----VDL 224

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DB 176 GAGAGARPCWEEFEDVWGRGIRP-QPWKQLCLELRAANGGPGAAEDBARPPGQPPPPDL 234
 QY 225 RGLGDRRAARQVHEKALFLVFGRTKRDLFENEIKAR----- 261
 DB 235 RSLGGERRRVTPQERLALVFFSSQKRTL-FAMERQQLSATEVVGPGGAGSGSPPPP 293
 QY 262 -----SGQDKTYEYELFSQRRRRAPLATROGKRPSKNIKARCSKALHVFCKMGMD 316
 DB 294 PPPPSPGTPDAGILMSP--SPGRRRRRFAFSRGRKRRGKSRRLCSKPLHVFKELGMD 351
 QY 317 WIIAPLEYEAFHCCEGICFEPRLSRSHLEPTNHAVIQTLNMGDPESPPTCCVPTRLSPISI 376
 DB 352 WIIAPLEYEAFHCCEGICFEPRLSRSHLEPTNHAVIQTLNMGDPESPPTCCVPTRLSPISI 411
 QY 377 LEIDSANNNVVKQYEDMNVESGCR 401
 DB 412 LYIDAGNNVNVNEEYEMVYESGCR 436

RESULT 4

GDF6_MOUSE STANDARD: PRT: 125 AA.
 ID GDF6_MOUSE
 AC P43028;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
 GN GDF6 OR GDF-6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE-Liver;
 RX MEDLINE-94195427; PubMed-8145850;
 RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
 RA Lee S.-J.;
 RT "Limb alterations in brachypodism mice due to mutations in a new
 member of the TGF beta-superfamily.";
 RL Nature 368:639-643(1994).
 CC -1- SIMILARITY: Homodimer; disulfide-linked (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
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 or send an email to license@sib-sib.ch).
 CC EMBL: U08338; AAA18779.1;
 DR EMBL: PIR: S43295; S43295.
 DR HSP: P12643; 3BMP.
 DR MGD: MGI:95689; Gdf6.
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-beta; 1.
 DR PRINTS: PRO0438; GFCYSKNOT.
 DR PRINTS: PRO0669; INHIBINA.
 DR PRODOM: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Growth factor; Cytokine; Glycoprotein.
 KW NON_TER
 FT PROPEP
 FT CHAIN
 FT DISULFID 6 125
 FT DISULFID 24 90
 FT DISULFID 53 122
 FT DISULFID 57 124
 FT DISULFID 89 89
 FT POTENTIAL.
 FT GROWTH/DIFFERENTIATION FACTOR 6.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT INTERCHAIN (BY SIMILARITY).

SQ SEQUENCE 125 AA; 14373 MW; 10FA2A5B7748DA32 CRC64;

Query Match 26.9%; Score 573; DB 1; Length 125;
 Best Local Similarity 79.2%; Pred. No. 3.8e-33;
 Matches 99; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 277 RRRRAPLATROGKRPSKNIKARCSKALHVFCKMGMDWIIAPLEYEAFHCCEGICFEP 336
 DB 1 RRRRRRFAFSRGRKRRGKSRRLCSKPLHVFKELGMDWIIAPLEYEAFHCCEGICFEP 60
 QY 337 LRSHLEPTNHAVIQTLNMGDPESPPTCCVPTRLSPISILEIDSANNNVVKQYEDMNV 396
 DB 61 LRSHLEPTNHAVIQTLNMGDPESPPTCCVPTRLSPISILEYIDAGNNVNVNEEYEMV 120
 QY 397 SGGCR 401
 DB 121 SGGCR 125

RESULT 5

GDF7_MOUSE STANDARD: PRT: 151 AA.
 ID GDF7_MOUSE
 AC P43029;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 7 precursor (GDF-7) (Fragment).
 GN GDF7 OR GDF-7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE-Liver;
 RX MEDLINE-94195427; PubMed-8145850;
 RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
 RA Lee S.-J.;
 RT "Limb alterations in brachypodism mice due to mutations in a new
 member of the TGF beta-superfamily.";
 RL Nature 368:639-643(1994).
 CC -1- SIMILARITY: Homodimer; disulfide-linked (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
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 CC EMBL: U08339; AAA18780.1;
 DR EMBL: PIR: S43296; S43296.
 DR HSP: P12643; 3BMP.
 DR MGD: MGI:95690; Gdf7.
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-beta; 1.
 DR PRINTS: PRO0438; GFCYSKNOT.
 DR PRODOM: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Growth factor; Cytokine; Glycoprotein.
 KW NON_TER
 FT PROPEP
 FT CHAIN
 FT DISULFID 6 151
 FT DISULFID 50 116
 FT DISULFID 79 148
 FT DISULFID 83 150
 FT DISULFID 115 115
 FT DISULFID 115 115
 FT DISULFID 1 5
 FT DOMAIN 16 41
 FT POTENTIAL.
 FT GROWTH/DIFFERENTIATION FACTOR 7.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT INTERCHAIN (BY SIMILARITY).
 FT POLY-ARG.
 FT POLY-GLY.

Miller D.A., Cecil J.D., Lock L.F., Lee A., Buchberg A.M.,
 Stachura L.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
 Verma N.A.,
 "Chromosomal localization of seven members of the murine TGF-beta
 superfamily suggests close linkage to several morphogenetic mutant
 loci."
 Genomics 6:505-520(1990).
 -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 -1- SUBUNIT: Homodimer; disulfide-linked.
 -1- SIMILARITY: Belongs to the TGF-beta family.

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 EMBL: I25602; AAB05665.1; -
 PIR: A34201; A34201.
 HSSP: P12643; 3BMP.
 MGD: MGI:88177; BMP2.
 DR GO: GO:0045165; P:cell fate commitment; IMP.
 DR GO: GO:0009790; P:embryonic development; IMP.
 DR GO: GO:0009887; P:organogenesis; IMP.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGF-propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 DR Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1
 FT PROPEP 20
 FT CHAIN 281
 FT DISULFID 294
 FT DISULFID 323
 FT DISULFID 327
 FT DISULFID 358
 FT CARBOHYD 134
 FT CARBOHYD 162
 FT CARBOHYD 198
 FT CARBOHYD 336
 FT CONFLICT 110
 FT CONFLICT 113
 FT CONFLICT 271
 SQ SEQUENCE 394 AA; 44514 MW; FDBAOF10587ED54 CRC64;
 Query Match 20.8%; Score 443.5; DB 1; Length 394;
 Best Local Similarity 32.8%; Pred. No. 1,2e-23;
 Matches 131; Conservative 48; Mismatches 118; Indels 103; Gaps 19;
 OY 42 SSELTKAREPGRERKEPRPPITPHHEMYSTKRTSLSDARKGNSV-----KLE- 95
 DB 58 SNEFLKOR-----PTREKDVVPP-----YMDLKR-----KHSQGGGAPAPRRRLR 100
 OY 96 -AGLANITTSF-----IDKGODRGPRVKKQRYVPDISALEKDGIL-GAELRIKKRPSD 148
 DB 101 AASRANTVRFPHOLEAVEELPEWMSGTAR--REFNLSVSPSEFTLSLDELIFRQIDE 158
 OY 149 T-----AKPAAPGGGAAOLKSSCSGPGAPASILDVRSVPGIDSGGWV 193
 DB 159 ALGNSSFOHRINIYEIIKPA-----AANLKF-----VYTR-----LDTRIYV-NONTISOWES 204
 OY 194 FDIWKLFERNKNSAQ-----LCLLEAEMRGRAVDLGLGFDRARAOVHE-----KAL 241
 DB 205 FGVPAVAVRMTTQCHTNGHFVVAHLEENPVSKRHV--RISRSIHQDEHSWQIRPL 261
 OY 242 FLVGGPRKKRDLFENEIKARSGODDKTVYEYLFSQRRKRRAPLAFQGRPKSKNKARCS 301
 DB 262 LVYTGHHGK-----GHPLKREKKQAKHKQR-----KRLKSSCK 295

302 KRALHNFKMGMDWIIAPLEAFHRCGLCEPPLRSHLEPTNNAVITQTLNMSKDPST 361
 DB 296 RHPLVYFSPVGNWMDVAPPGYHAFYCGCEPFLADHNTSTNAIVQTLNVSFN-SKI 354
 OY 362 PPTCCVPTRLSPISILIFDSANNVYKQEDWVESCGR 401
 DB 355 FKACVPTFLSMTLYIDENKRYVLKNTQDMWVECGCR 394
 RESULT 8
 ID BMP2_RAT STANDARD; PRT; 393 AA.
 AC P49001:
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2a).
 GN BMP2 OR BMP-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP TISSUE=bone;
 RC Feng J.Q., Chen D., Feng M., Harris M.A., Mundy G.R., Harris S.E.;
 RA Submitted (SEP-1993) to the EMBL/GenBank/DDI databases.
 RL -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.

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 EMBL: Z25868; CA81088.1; -
 PIR: S37073; S37073.
 HSSP: P12643; 3BMP.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR00111; TGFb.N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGF-propeptide; 1.
 DR PRINTS: PR00669; INHIBIN.
 DR PRODOM: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF-BETA_1; 1.
 DR Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1
 FT PROPEP 20
 FT CHAIN 281
 FT DISULFID 293
 FT DISULFID 322
 FT DISULFID 326
 FT DISULFID 357
 FT CARBOHYD 133
 FT CARBOHYD 161
 FT CARBOHYD 197
 FT CARBOHYD 335
 SQ SEQUENCE 393 AA; 44383 MW; 7D20865852E0F213 CRC64;
 Query Match 20.7%; Score 440.5; DB 1; Length 393;
 Best Local Similarity 31.7%; Pred. No. 1,9e-23;
 Matches 133; Conservative 54; Mismatches 131; Indels 101; Gaps 19;
 OY 37 AGVPSSEFLKAREPGRPREP-----RPP-----TPHEHYMSLY 77


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FT STRAND 328 328
FT TURN 331 332
FT STRAND 339 339
FT HELIX 341 352
FT TURN 354 355
FT STRAND 361 374
FT TURN 376 377
FT STRAND 380 396
SQ SEQUENCE 396 AA; 44702 MW; 20653A3987B25E60 CRC64;

Query Match 20.6%; Score 440; DB 1; Length 396;
Best Local Similarity 31.7%; Pred. No. 2.1e-23;
Matches 126; Conservative 54; Mismatches 121; Indels 96; Gaps 17;

QY 42 SFFLLKRRPGRPPREPPRPITPHEYMSTYRTIS-DADRRGSSVYLEGLAN 100
DB 59 SMFGLK--GRPTSRDAVVP-----PYMLDLYRRHSGGSGSPAPDRRLERASRN 107
QY 101 TITSF-----IDGDDRGVYVVKORYYFDISAL-EKDGILGELILKRRKSDT----- 149
DB 108 TVASFHHEESLELPETSGKTR--RFFNLSISIPFEETISAEIQVFEQMDALGNS 165
QY 150 -----AKPAAPGGGAAOLKLSGSPGROPASILDVRSYVGLDGGSEVFDIK 198
DB 166 SFHRINIEYLIKPAVAN-----SKFPYTR--LLDTRLV-NQNASRMSFDVTP 211
QY 199 LFRNFNSAO-----LCLELAWERGRAVDLRGLGFDRAQVHE-----KALPLV 244
DB 212 AVMRW--TAQGHANHFVVEVAHLEKQGVSKRHV---RISKSLQDEHMSQIRPLVT 266
QY 245 FGRTRKRDLEFNDIKARSGODKTYEYLFSSQRRRAPLATRQCKRPSKRLKARCSRA 304
DB 267 FGHDKG-----GHLHRKRRKQAKHQR-----KRLKSSCKRHP 300
QY 305 LHVNRKMGMDMIAPLEAEFAHCEGLCEPFLRSHLEPTNNAVOTLANSMDPESTPT 364
DB 301 LYVDSVDGVMWMIYAPPGYHAFYCHGECPEPLADHLNSTHNAVOTLVNSVN-SKIKR 359
QY 365 CCVPTLSPISILFIDSANNVYKQYEDMVVSGCGR 401
DB 360 CCVPTLSAISMLYDENEKVYLKNYODMVVSGCGR 396

RESULT 10
BMP2_RABIT STANDARD: PRT; 395 AA.
AC 046564;
DB 15-JUL-1999 (Rel. 38, Created)
DB 15-JUL-1999 (Rel. 38, Last sequence update)
DB 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 2 precursor (BMP-2).
GN Oryctolagus cuniculus (Rabbit).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-New Zealand white; TISSUE-Ocular ciliary epithelium;
RA Wan X.L., Sears J., Chen S., Sears M.;
RT Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
RT epithelium.
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
CC -1- SUBUNIT: Homodimer; disulfide-linked (BY similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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DB EMBL: AF041421; AAB96785.1; -.
DR HSP: P12643; 3BMP.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00669; INHIBIN.
DR PRODOM: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_beta_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 23
FT PROPE 24 281
FT CHAIN 282 395
FT DISULF 295 360
FT DISULF 328 392
FT DISULF 328 394
FT CARBOHYD 359 359
FT CARBOHYD 134 134
FT CARBOHYD 199 199
FT CARBOHYD 337 337
SQ SEQUENCE 395 AA; 44664 MW; 8D1DCFBAC582496 CRC64;

Query Match 20.6%; Score 439; DB 1; Length 395;
Best Local Similarity 31.1%; Pred. No. 2.5e-23;
Matches 129; Conservative 58; Mismatches 128; Indels 100; Gaps 19;

QY 30 GCKAPRAGVSSFFLLKRAEPGRPPRPITPHEYMSTYRTISDADRRGKN 89
DB 38 GRSPQPSDLDLSEFLRLSMGLKQRP--TPSDAVVVP--TWLDLYR-----RHSG 88
QY 90 SVV-----KLE--AGLANTTSF-----IDGDDRGVYVVKORYYFDISAL-EKDGILG 136
DB 89 PGADPDRRLERASRNANVRSFHERSLELPETSGKTR--RFFNLSISIPFEETIS 146
QY 137 AEILRLKRRKSDT-----AKPAAPGGGAAOLKLSGSPGROPASILDV 180
DB 147 AELQVFEQMDALGDDSGFHHRIINIEYLIKPAVAN-----SKFPATR--LLDT 193
QY 181 RSVPLGDSGEVFDIWKLFERNKNSAO-----LCLELAWERGRAVDLRGLGFDRAAR 234
DB 194 RLV-NQNTSRMSFSDVTPAVMRW--TAQGHANHFVVEVAHLEKQGVSKRHV---RISK 247
QY 235 QVHE-----KALPLVFGRTKRDLEFNEIKARSGODKTYEYLFSSQRRRAPLAT 286
DB 248 SLHPDEHMSQIRPLVTFGCHK-----GHLHRKRRKQAKHQR 287
QY 287 RQCKRPSKRLKARCSRALHVNFKMGMDMIAPLEAEFAHCEGLCEPFLRSHLEPTNH 346
DB 288 R-----KRLKSSCKRHPLYVDFSDGVMWMIYAPPGYHAFYCHGECPEPLADHLNSTH 341
QY 347 AVIQTLMNSMDPESTPTCCVPTLSPISILFIDSANNVYKQYEDMVVSGCGR 401
DB 342 AIVOTLVNSVN-SKIPRACCVPTLSAISMLYDENEKVYLKNYODMVVSGCGR 395

RESULT 11
BMP2_DANDA STANDARD: PRT; 396 AA.
AC 019006;
DB 15-JUL-1998 (Rel. 36, Created)
DB 15-JUL-1998 (Rel. 36, Last sequence update)
DB 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 2 precursor (BMP-2).
GN BMP2.
OS Dama dama (Fallow deer) (Cervus dama).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=30532;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Antler;
RA MEDLINE=97157076; PubMed=9003457;
RX Feng J.O., Chen D., Ghosh-Choudhury N., Esparza J., Mundy G.R.,
RA Harris S.E.;
RT "Bone morphogenetic protein 2 transcripts in rapidly developing deer
RT antler tissue contain an extended 5' non-coding region arising from a
RT distal promoter."
RL Blochim. Biophys. Acta 1350:47-52(1997).
CC -1- SUBUNIT: INDICES CARTILAGE AND BONE FORMATION.
CC -1- SIMILARITY: Homodimer; disulfide-linked.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
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CC
DR EMBL: AJ001817; CAA05033.1;
DR HSSP: P12643; 3BMP.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PRO0669; INHIBIN.
DR PRODOM: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA.1; 1.
KW Signal; growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL. 1 23
FT PROPEP 24 282
FT CHAIN 283 396
FT DISULFID 296 361
FT DISULFID 325 393
FT DISULFID 329 395
FT DISULFID 360 360
FT CARBOHYD 135 135
FT CARBOHYD 163 163
FT CARBOHYD 164 164
FT CARBOHYD 200 200
FT CARBOHYD 338 338
SQ SEQUENCE 396 AA; 44646 MW; 5FE23A0AC7F91572 CRC64;
Query Match 20.3%; Score 433; DB 1; Length 396;
Best Local Similarity 30.4%; Pred. No. 6, 5e-23;
Matches 128; Conservative 51; Mismatches 132; Indels 110; Gaps 16;
OY 29 PGKAPPRKAGVSPSSFLKKAREPPRRPPPTPIPHMYMLSTRTLS-DADRGG 87
DB 38 PERSSQPDVDVLSSEFLRLSMFLGKQRP-TPSRPVVPP-YMDLRLHSGOGAPDA 94
OY 88 GNSVYKLEAGLANTITSE-----IDKGODRGVVAKORYVDISAL-EKDGILGALRI 141
DB 95 PGHRLERASLANVTATFHHESELEBELPMSEKTRR-RFFNLTSTPIPEEFTLSALQV 152
OY 142 LKKKDSY-----AKPAAPGGGAAQLKLSSCPSPGRASILLDVRSVPG 185
DB 153 FKKHMEPELENNSSFHRIINFEIILKPAVAN-----SKFPVTR-----LLDPLAVT- 198
OY 186 LGSQGEVEVDIKLFRNFKNASQCLELEAMERGRAVDLRLGCF----- 229
DB 199 QNASRRESFDV-----TPAVKMTAAGLTHNGEVVEVAHPEDSYGASKR 242
OY 230 -PRAARQVE-----KALFLVGRTRKRLDFENEIKARSGODKTYEYLLSQRRR 280
DB 243 HVRISLSLHGDHSMQIRPLVLTGCHDK-----GPHLRKRKR 282
OY 281 RAPLATRCKRPSKLNKARCSRKALHVNPKDMGMDWITIAPLEYEAHFCEGLCEPFLSH 340

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DB 283 QAKHKQR-----KRLKSSCKRRHPLYVDSDVGMDMDWITIAVAPGYNAFYCHGCGPEPLADH 336
OY 341 LEPTNAVIQTLNMSNDPESTPTCCVPRRLSPISILFIDSANNVYKQEMVWYSSCGC 400
DB 337 LNSTNAIVQTLVNSVN-SKIRACCVPELSAISMLYIDENKRYLKANTQDMVWYSGCC 395
OY 401 R 401
DB 396 R 396
RESULT 12
BMP4_CHICK
ID BMP4_CHICK STANDARD; PRT; 405 AA.
AC 090752;
DT 01-NOV-1997 (Rel. 35, Last Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 4 precursor (BMP-4).
GN BMP4 OR BMP-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=White Leghorn;
RX MEDLINE=94163974; PubMed=8119128;
RA Francis P.H., Richardson M.R., Brickell P.M., Tickle C.;
RT "Bone morphogenetic proteins and a signalling pathway that controls
RT patterning in the developing chick limb."
RL Development 120:209-218(1994).
RN [2]
RP FUNCTION.
RX MEDLINE=99128179; PubMed=9927590;
RX Pizette S., Niswander L.;
RT "Bmps negatively regulate structure and function of the limb apical
RT ectodermal ridge."
RL Development 125:883-894(1999).
CC -1- FUNCTION: NEGATIVELY REGULATES THE STRUCTURE AND FUNCTION OF THE
CC LIMB APICAL ECTODERMAL RIDGE.
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SIMILARITY: Belongs to the TGF-beta family.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X75915; CAA53514.1;
DR PIR: I50608; I50608.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRODOM: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA.1; 1.
KW Signal; growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL. 1 19
FT PROPEP 20 291
FT CHAIN 292 405
FT DISULFID 305 370
FT DISULFID 334 402
FT DISULFID 338 404
FT DISULFID 369 369
FT CARBOHYD 144 144

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Thu Aug 28 08:27:34 2003

us-09-901-556c-3.rsp

Page 12

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Db      225  WTREKOPNHGLAVEVTHFHHTRTFHOGHVRL-----SRSILQSGDMAQFRPILVT 275
QY      262  SGODDKTYEYLFSQRRRRAPLATROGRRPSKNLKARCSRRKALHVNFKDGMDDWITAP 321
Db      276  FGHGDRG-----HALTRRRRAKRSCLKHHPQARAKKNKCRRHLYVDESDVGMNDWIVAP 330
QY      322  LEYAFHCEGLCEPPLREHLEPTNHAVIQTLNLSMDPESTPPTCCVPTRLSPISITFTDS 381
Db      331  PGYQAFYCHGDCPEPLADHFNSTNHAIYQTLVNSVN-SSIPKACCVPTELTSISMLTYDE 389
QY      382  ANNVYKQYEDMVYESGCCR 401
Db      390  YDKVYLNKYQEMVYEGCCR 409
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Search completed: August 19, 2003, 10:28:44
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2003, 10:25:21 ; Search time 101 Seconds

(without alignments)
1024.545 Million cell updates/sec

Title: US-09-901-556c-3

Perfect score: 2133
Sequence: 1 PGGPPKRPCHPPQTRQATAR.....ANNVYKQYEDMVESGCCR 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTRMBL.23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organella:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	1597.5	74.9	500	13	09W6G0
2	1433	67.2	324	11	09YHW9
3	1395	60.7	249	11	08BRW9
4	989	46.4	257	13	042303
5	900	42.2	399	13	09W753
6	893.5	41.9	413	13	09DGN4
7	844.5	39.6	412	7	012938
8	757.5	35.5	447	6	09BDW8
9	648.5	30.4	441	11	099MK1
10	643.5	30.2	261	13	09W6C0
11	625.5	29.3	294	6	09BDW9
12	567.5	26.6	126	13	093573
13	466.5	21.9	403	13	08JIT8
14	465.5	21.8	403	13	08JIT6
15	464.5	21.8	403	13	08JIT0
16	463.5	21.7	403	13	08JIT3

17	462.5	21.7	403	13	08JIT2	08JIT2 astatoreoch
18	459.5	21.5	403	13	08JIT5	08JIT5 oreochromis
19	458.5	21.5	403	13	08JIT2	08JIT2 boulengeroc
20	458.5	21.5	403	13	08JIT1	08JIT1 ctenochromi
21	458.5	21.5	403	13	08JIT2	08JIT2 tilapia ren
22	456.5	21.4	403	13	08JIT4	08JIT4 steatocranu
23	455.5	21.4	400	13	057574	057574 brachydanio
24	454.5	21.3	403	13	08JIT0	08JIT0 cyprichromi
25	454.5	21.3	403	13	08JIT7	08JIT7 julidochrom
26	454	21.3	411	5	09U418	09U418 branchiost
27	452	21.2	417	5	09YX07	09YX07 lytechinus
28	447	21.0	398	13	090YD7	090YD7 xenopus tro
29	445	20.9	405	5	0905E8	0905E8 ptychodera
30	444	20.8	361	5	096504	096504 branchiost
31	439.5	20.6	400	13	013107	013107 brachydanio
32	437.5	20.5	422	5	08IAE3	08IAE3 stichopus j
33	437	20.5	411	13	093369	093369 brachydanio
34	431.5	20.2	364	13	09PVK1	09PVK1 gallus gall
35	431.5	20.2	509	5	08WS99	08WS99 archaster t
36	431	20.2	411	13	057573	057573 brachydanio
37	430.5	20.2	461	5	08MXZ3	08MXZ3 hemlentrot
38	428.5	20.1	453	13	P87373	P87373 gallus gall
39	427.5	20.0	391	13	08UVO8	08UVO8 brachydanio
40	427.5	20.0	391	13	08UVO2	08UVO2 brachydanio
41	427.5	20.0	391	13	090YJ3	090YJ3 brachydanio
42	424.5	19.9	454	11	08CCE0	08CCE0 mus musculu
43	422	19.8	386	13	013109	013109 brachydanio
44	421	19.7	400	13	090YD6	090YD6 xenopus tro
45	420	19.7	301	5	097390	097390 crassostrea

ALIGNMENTS

RESULT 1

ID	09W6G0	PRELIMINARY;	PRT;	500 AA.
AC	09W6G0;			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	GDF-5 protein.			
GN	GDF5.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID-9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-99146893; PubMed-10021348;			
RA	Francis-West P.H., Abdelfattah A., Chen P., Allen C., Parish J.,			
RA	Ladher R., Allen S., Macpherson S., Luyten F.P., Archer C.W.;			
RT	"Mechanisms of GDF-5 action during skeletal development."			
RT	Development 126:1305-1315(1999).			
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
DR	EMBL: AF123389; AAD30451.1; -			
DR	HSSP: P12643; 3BMP.			
DR	InterPro: IPR002400; GF_cyskn0t.			
DR	InterPro: IPR002405; Inhibin_alpha.			
DR	InterPro: IPR001839; TGFb.			
DR	InterPro: IPR001111; TGFb_N.			
DR	Pfam: PF000019; TGF-beta.1.			
DR	Pfam: PF00688; TGF-beta.1.			
DR	PRINTS: PR00438; GFCISKN0T.			
DR	PRINTS: PR00669; INHIBINA.			
DR	SMART: SM00204; TGFb.1.			
DR	SMART: PS00250; TGF-beta.1.			
DR	PROSITE: PS00250; TGF-beta.1.			
DR	SEQUENCE 500 AA; 55952 MW; 1DE8385A3119A598 CRC64;			

Query Match 74.9%; Score 1597.5; DB 13; Length 500;
Best Local Similarity 78.3%; Pred. No. 1.4e-129;

Matches 314; Conservative 23; Mismatches 57; Indels 7; Gaps 3;

OY 5 EPKGGPPTROTARTATVPKRGOLPGKAPPK-----AGSVSPSSFLTKKAREGPREPREKE 60
 DB 103 EAKVGHLP-SRPSAVRTVPKPNVSGSKAAALKTKTGGDASFTFKTKTKPREKRE 161
 OY 61 PEPRPPTPEHYMLSLYRTLSADNRKGSVYKLAGLANTTSTFDKGGDRPVYRKQ 120
 DB 162 TFSRPPTPEHYMLSLYRTLSADNRKGSVYKLAGLANTTSTFDKGGDRPVYRKQ 221
 OY 121 RYVPDISALEKODLGAELRIILKKPSDTAKPAGGCGAAOLKISSCPGSPASILDV 180
 DB 222 KYTFDISALEKODLGAELRIILKKPSDTAKPAGGCGAAOLKISSCPGSPASILDV 279
 OY 181 RSVPGLDGSGMEVFDIMKLFRRNKNASQICLELEAMERGAVDLRGIGFDBAARQVHEKA 240
 DB 280 RTVSTIDTPKMEVFDIMKLFRRNKNASQICLELEAMERGAVDLRGIGFDBAARQVHEKA 339
 OY 241 LFLVFGRTKKRDLFENEIKARSGODDKTYEYLFQSRKRRAPLATROGKSPSKNLKARC 300
 DB 340 LFLVFGRTKKRDLFENEIKARSGODDKTYEYLFQSRKRRAPLATROGKSPSKNLKARC 399
 OY 301 SRKALHVNFKMDGMDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNNAVYOTLMSNDPES 360
 DB 400 SRKALHVNFKMDGMDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNNAVYOTLMSNDPES 459
 OY 361 TTPPCCVPTLSPISLIFIDSANVYKQYEDMVESGCCR 401
 DB 460 TTPCCVPTLSPISLIFIDSANVYKQYEDMVESGCCR 500

RESULT 2

OY Q9YHW9 PRELIMINARY; PRT: 324 AA.
 ID Q9YHW9
 AC Q9YHW9; 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Growth differentiation factor 5 (Fragment).
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RC SEQUENCE FROM N.A.
 RK TISSUE=Leg bud;
 RX MEDLINE=9119368; PubMed=918693;
 RA Medline R., MacIas D., Ganan Y., Economides A.N., Wang X., Wu Q.,
 RA Stahl N., Sampath K.T., Varona P., Hurler J.M.;
 RT "Expression and function of Gdf-5 during digit skeletogenesis in the
 RT embryonic chick leg bud."
 RL Dev. Biol. 206:33-45(1999).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AF075441; AAD14568.1; -
 DR HSSP: P12643; 3BMP.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; TGF.
 DR Pfam: PF000019; TGF-beta.1.
 DR Pfam: PF00668; TGF-propeptide.1.
 DR PRINTS: PR00669; INHIBIN.
 DR PRODOM: PD000357; TGF.1.
 DR SMART: SM00204; TGF.1.
 DR PROSITE: PS00250; TGF_BETA.1; 1.
 FT NON_TER 1
 FT 324
 SO SEQUENCE 324 AA; 37206 MW; 08BA7CB11375007 CRC64;

Query Match 67.2%; Score 1433; DB 13; Length 324;
 Best Local Similarity 83.7%; Pred. No. 1.3e-115;
 Matches 273; Conservative 21; Mismatches 30; Indels 2; Gaps 1;

OY 67 ITPHEHYMLSLYRTLSADNRKGSVYKLAGLANTTSTFDKGGDRPVYRKQVYVDI 126
 DB 1 ITPHEHYMLSLYRTLSADNRKGSVYKLAGLANTTSTFDKGGDRPVYRKQVYVDI 60
 OY 127 SAELEDGLGAELEIRKRRKPSDTAKPAGGCGAAOLKISSCPGSPASILDVSYGCL 186
 DB 61 SAELEDGLGAELEIRKRRKPSDTAKPAGGCGAAOLKISSCPGSPASILDVSYGCL 218
 OY 187 DCGMEVFDIMKLFRRNKNASQICLELEAMERGAVDLRGIGFDBAARQVHEKALFLVG 246
 DB 119 DTPKMEVFDIMKLFRRNKNASQICLELEAMERGAVDLRGIGFDBAARQVHEKALFLVG 178
 OY 247 RTKKRDLFENEIKARSGODDKTYEYLFQSRKRRAPLATROGKSPSKNLKARC 306
 DB 179 RTKKRDLFENEIKARSGODDKTYEYLFQSRKRRAPLATROGKSPSKNLKARC 238
 OY 307 VNFKMDGMDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNNAVYOTLMSNDPESPTTCC 366
 DB 239 VNFKMDGMDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNNAVYOTLMSNDPESPTTCC 298
 OY 367 VPTRLSPISLIFIDSANVYKQYED 392
 DB 299 VPTRLSPISLIFIDSANVYKQYED 324

RESULT 3

OY Q8BRW9 PRELIMINARY; PRT: 249 AA.
 ID Q8BRW9
 AC Q8BRW9; 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Growth differentiation factor 5 (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RK STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium;
 RA The RIKEN genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL: AK041168; BAC30847.1; -
 FT NON_TER 1
 FT 249
 SO SEQUENCE 249 AA; 28409 MW; E6EA047F06B57189 CRC64;

Query Match 60.7%; Score 1295; DB 11; Length 249;
 Best Local Similarity 96.8%; Pred. No. 7.6e-104;
 Matches 241; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 153 AAPGGGAAOLKISSCPGSPASILDVRSVPGLDGSGMEVFDIMKLFRRNKNASQICLE 212
 DB 1 AVPSGGAOLKISSCPGSPASILDVRSVPGLDGSGMEVFDIMKLFRRNKNASQICLE 60
 OY 213 LEAMERGAVDLRGIGFDBAARQVHEKALFLVGRTKKRDLFENEIKARSGODDKTYEY 272
 DB 61 LEAMERGAVDLRGIGFDBAARQVHEKALFLVGRTKKRDLFENEIKARSGODDKTYEY 120
 OY 273 LFSORRRRAPLATROGKSPSKNLKARC 332
 DB 121 LFSORRRRAPLATROGKSPSKNLKARC 180
 OY 333 CEPPLRSHLEPTNNAVYOTLMSNDPESPTTCCVPTRLSPISLIFIDSANVYKQYED 392
 DB 181 CEPPLRSHLEPTNNAVYOTLMSNDPESPTTCCVPTRLSPISLIFIDSANVYKQYED 240
 OY 393 MVESGCCR 401
 DB 241 MVESGCCR 249

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RESULT 4
ID 042303 PRELIMINARY; PRT; 257 AA.
AC 042303;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Contact (Fragment).
GN GDF5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97398455; PubMed=9256353;
RA Bruneau S., Mourrain P., Rosa F.M.;
RT "Expression of contact, a new zebrafish DVR member, marks mesenchymal
RT cell lineages in the developing pectoral fins and head and is
RT regulated by retinoic acid."
RL Mech. Dev. 65:163-173(1997).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: Y12005; CAA72733.1; -.
DR HSSP: P12643; 3BMP.
DR ZFIN: ZDB-GENE-990415-39; gdf5.
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001839; TGFb.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00669; INHIBINA.
DR PRODOM: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
FT NON_TER 1
FT CHAIN 140 257 POTENTIAL.
SQ SEQUENCE 257 AA; 29787 MW; 6D64F0542F948849 CRC64;

Query Match 46.4%; Score 989; DB 13; Length 257;
Best Local Similarity 71.6%; Pred. No. 2.2e-77;
Matches 187; Conservative 25; Mismatches 45; Indels 4; Gaps 2;

QY 141 ILRRKSDPAKPAAPGGRAAOLKLSGPGROPASILDVRSVPGDLSGSEVFDIMKLF 200
DB 1 ILRRKSDPAKPAAPGGRAAOLKLSGPGROPASILDVRSVPGDLSGSEVFDIMKLF 58
QY 201 RNFKNASQALCLEANERGRAVDLRGLGFDRAARQVHEKALFLVFGTRKKRDLEFFMEIKA 260
DB 59 KNRNRPQCLLELDVADHGRPLDLRLGLSIRAGQREKAFVYVFGTRKKRGLFEYMEIKA 118
QY 261 RSGQDDKTYEYELFSQRRRRAPLATROGRRPSKLNKARCSKALVNFDMQWDWMTIA 320
DB 119 RSHDHDKTYEYELFSQRRRRAPLATROGRRPSKLNKARCSKALVNFDMQWDWMTIA 176
QY 321 PLEYEAFHCGELCEPFLRSHLEPTNNAVIQTLNMSMDPESTPTCCVPTLSPISILFD 380
DB 177 PLEYEAFHCGELCEPFLRSHLEPTNNAVIQTLNMSMDPESTPTCCVPTLSPISILFD 236
QY 381 SANNNVYKQYEDMVESCGCR 401
DB 237 SANNNVYKQYEDMVESCGCR 257

RESULT 5
ID 09W753 PRELIMINARY; PRT; 399 AA.
AC 09W753;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

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DE Growth and differentiation factor 6.
GN GDF6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99396700; PubMed=10393114;
RA Chang C., Hemmati-Britvanlou A.;
RT "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs."
RL Development 126:3347-3357(1999).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF155125; AAD38402.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00669; INHIBINA.
DR PRODOM: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
SQ SEQUENCE 399 AA; 45571 MW; C549D973B50B8517 CRC64;

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Query Match 42.2%; Score 900; DB 13; Length 399;
Best Local Similarity 47.7%; Pred. No. 2e-69;
Matches 185; Conservative 71; Mismatches 90; Indels 42; Gaps 12;

QY 39 SVPSFLFKKAREGPPREPKE-----PFRPPITPHEYMLSTRTSDAD 84
DB 29 SVPSFLFKKAREGPPREPKE-----PFRPPITPHEYMLSTRTSDAD 82
QY 85 RKGNSSVKLEAGLANTITTSFIDKQDDRG-PVVRKORYVEDISAL-EKDGLGAELRIL 142
DB 83 KLGINSFPPSSASANTISSFVDRRDNLSLPILKRRKYLFDVSTLSKDELVGAELRVF 142
QY 143 RKRPSDTAKPAAPGGRAAOLKLSGPGROPASILDVRSVPGDLSGSEVFDIMKLF 201
DB 143 RKRPSDTAKPAAPGGRAAOLKLSGPGROPASILDVRSVPGDLSGSEVFDIMKLF 195
QY 202 NF-KNSAQCLLEDA--WENGRVAVDLRGIGFDRAARQVHEKALFLVFGTRKKRDLEFFMEI 258
DB 196 DISQKKQICVELKALSLTGTLEVNLRSLGLARRPSHQKALLVFTKSSRNLYNEL 254
QY 259 K-----ARSGQDDKTYEYELFSQRRRRAPLATROGRRPSKLNKARCSKALVNFDMQ 313
DB 255 KEQVHSSKSKMEKARLH---FKTRRRRTTFNRRHGRHRRKRLKSKPLVNFKEIG 311
QY 314 WDMWITAPLEYEAFHCGELCEPFLRSHLEPTNNAVIQTLNMSMDPESTPTCCVPTLSP 373
DB 312 WDMWITAPLEYEAFHCGELCEPFLRSHLEPTNNAVIQTLNMSMDPESTPTCCVPTLSP 371
QY 374 ISLIFDSANNNVYKQYEDMVESCGCR 401
DB 372 ISLIFDSANNNVYKQYEDMVESCGCR 399

RESULT 6
ID 09DGN4 PRELIMINARY; PRT; 413 AA.
AC 09DGN4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Growth/differentiation factor 16 precursor protein.
GN GDF16.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC	Amphiblatrachia:	Anura; Mesobatrachia; Pipoidae; Pipidae;
OC	Xenopodidae:	Xenopus.
OX	NCBI_TaxID=6355;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20368184;	pubmed=10906478;
RA	Vokes S.A., Kriegl P.A.;	
RT	Tcf16, a novel member of the growth/differentiation factor subgroup	
RT	of the TGF-beta superfamily, is expressed in the hindbrain and	
RT	epibranchial placodes.";	
RL	Mech. Dev. 95:279-282(2000).	
CC	-	SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR	EMBL: AF239676; AAF99597.1;	-
DR	HSSP: P12643; 3BMP.	
DR	InterPro: IPR002400; GF_cyanknot.	
DR	InterPro: IPR001839; TGFb.	
DR	InterPro: IPR001111; TGFb.N.	
DR	Pfam: PF000019; TGF-beta.1.	
DR	Pfam: PF006688; TGFb.poreptide.1.	
DR	PRINTS: PR00438; GRCYSKNOT.	
DR	ProDom: PD000357; TGFb.1.	
DR	SMART: SM00204; TGFb.1.	
DR	PROSITE: PS00250; TGF-BETA_1; 1.	
KW	SIGNAL.	
FT	SIGNAL.	
QO	SEQUENCE	413 AA; 23 POTENTIAL. 5FLI8D7D97E591P6 CRC64;

Query Match	41.9%;	Score 893.5;	DB 13;	Length 413;
Best Local Similarity	49.38;	Pred. No. 7.6e-69;		
Matches 185; Conservative	57;	Mismatches 98;	Indels 35;	Gaps 9

[illegible]

RESULT	7
012938	
ID	012938
AC	012938;
DT	01-JUL-1997 (TREMBLrel. 04, Created)
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	Dynamo protein precursor.
GN	GDF6A OR DYNAMO.
OS	Brachydanio rerio (Zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.

XX	NCBI_TaxID=7955;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Embryo;		
RX	MEDLINE=97231294; PubMed=9076689;		
RA	Birneau S., Rosa F.;		
RT	"Dnmo a new zebrafish DVR member of the TGF-B superfamily is		
RT	expressed in the posterior neural tube and is up regulated by Sonic		
RT	heghehog.";		
RL	Mech. dev. 61:199-212(1997).		
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.		
DR	EMBL: X99769; CA68102.1; -.		
DR	HSP; P12643; 3BMP		
DR	ZFIN: ZDB-GENE-980526-442; gdfca.		
DR	InterPro: IPR002400; GF_cysknct.		
DR	InterPro: IPR002405; Inhibin_alpha.		
DR	InterPro: IPR001839; TGFb.		
DR	InterPro: IPR001111; TGFb_N.		
DR	Pfam: PF000019; TGF-beta; 1.		
DR	Pfam: PF00688; TGFb_propeptide; 1.		
DR	PRINTS: PR00438; GFCYSKNCT.		
DR	PRINTS: PR00669; INHIBIN.		
DR	ProDom: PD000357; TGFb: 1.		
DR	SMART: SM00204; TGFb: 1.		
DR	PROSITE; PS00250; TGF_BETA_1; 1.		
KW	Signal.		
FT	SIGNAL	17	POTENTIAL.
FT	CHAIN	293	412
Q0	SEQUENCE	412 AA; 47072 MW; 4076E262C4481121 CRC64;	

Query Match	39.6%;	Score 844.5;	DB 13;	Length 412;
Best Local Similarity	50.0%;	Pred. No. 1.3e-64;		
Matches 179;	Conservative 56;	Mismatches 82;	Indels 41;	Gaps 12

Qy	67	ITHEWMLSIKRTLSADBRKGNSSVKIEAGLANTTISFIDKGGDD--KGPVYKROYF	124
Db	73	IEPHDWIMSTIKTFSAAEKRLGNASSFPSSKQAAVNTTISFDEGGDHLNSPLIK--OKYLE	131
Qy	125	DISAL--EKQGLIGAEIRLIK--KPSDITKPAAPGGGAOLKISSCSGROPSALIDVRS	182
Db	132	DVSTISENVEILIGAEIRITTKTISGFSRASEGP-----VEQLLISC-----QSHFTYDST	182
Qy	183	VPGLDG--SGWEYFDIWKLF--NFKSAOLCIELEAA--EKGRAVDLRIGLGFDPRAAO	235
Db	183	LDIEDAHKRMFEYFDWELFKERQHSIGNRFLCETLRDTLDPREKIDYLDLFFHHNGRP	242
Qy	236	VHKALFLVYGRTRKRDLEFNEIKARS---GQD-----DKTYEYELISQRRKRAP	283
Db	243	QIKKALLVYFTSKSQSLFEYERKKIKLWGLDSTIGKERSHST-----RBSRRRA	294
Qy	284	LATRGGRPSKNIKARCSKRALHVNFKMGWMDMIITAPLEYAFHCGICEPLRSHLEP	343
Db	295	LPRHRRKRRGKSKSKSRKPLHVNFRRLGMDWVIAPLDEYAHCGMCDFLRSHLEP	354
Qy	344	TNHAVTIOTLANSMDPESTPTCCVPTRLSPISLIFIDSAANVYVKQYEDMYVSSCCR	401
Db	355	TNHAIIOTLANSNPNMPPSCCVYSKISPLISILYIDAGNNVYVKQYEDMYVSSCCR	412

RESULT	8
Q9BDW8	
ID	Q9BDW8
AC	Q9BDW8
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE	Growth/differentiation factor 7.
GN	GDF7.
OS	Cercopithecus aethiops (Green monkey) (Primate).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC	Cercopithecinae; Cercopithecus.
NCBI	TaxID=9534;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21136583; PubMed-11238730;
 RA Watahabe A., Fujita H., Hayashi M., Yamamori T.;
 RT "Growth/differentiation factor 7 is preferentially expressed in the
 RT primary motor area of the monkey neocortex."
 RL J. Neurochem. 76:1455-1464(2001).
 CC -1- SIMILARITY: BELONGS TO THE TGF- β FAMILY.
 DR EMBL; AF254569; AAK30842.1; JOINED.
 DR HSSP; P12643; 3BMP.
 DR InterPro; IPR001839; TGF β .
 DR InterPro; IPR001111; TGF β .N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF β -propeptide; 1.
 DR ProDom; PD000357; TGF β ; 1.
 DR SMART; SM00204; TGF β ; 1.
 DR PROSITE; PS00250; TGF- β 1; 1.
 SQ SEQUENCE 447 AA; 4686 MW; DF46D591925A8391 CRC64;

Query Match 35.5%; Score 757.5; DB 6; Length 447;

Best Local Similarity 40.6%; Pred. No. 4.8e-57;
Matches 176; Conservative 65; Mismatches 131; Indels 61; Gaps 12;

QY 15 RQATARTV-TPKQLPGKAPPK--AGVPSSEFLKKAREPGPREPPPTTPH 70
 DB 30 RAAGAGPVPSPGGGGGGRTLAAGAAVPAAY--SRAPRRAAGSGFRNGSVPH 86
 QY 71 EYMLSYRTLSADRKGNSSVLEAGLANTITSFIDKGDDGPVVRKQRYVEDISAL- 129
 DB 87 HFMSLYRSLAGRAPAGAVAVSSSGHGRADDTTGTQATQDESAAETQSFLEVDSSLA 146
 QY 130 EKDGILGAEILRLKKPSDTAKPAAPGGGAAQ--LKLSCPSGROPASLIDVRSVPGI 186
 DB 147 DADVEYVGAELVRLRRSSPE-----PGSSSTSPILLSTGCGAARRLIXSRAEPI 200
 QY 187 DSGWEVFDIKLFRNFKNSAQ---LCLELEMERGRAVD-----LRGIGF--DR 231
 DB 201 VQGRWVEFVADAMRRHRRPRPPRAFCILL-----RAVTGVPRLSLRLRGFGMPG 254
 QY 232 AAROVEKALFLVFGRTKRDLEFNEIKARS-----GQDKTYVEYELFSG 276
 DB 255 GGSAPERALLVSSRTQKESLFEMRAQARALGALAAQPPDPGTGSGRAVYAGR 314
 QY 277 RRRRRAPLATR-----QGRKPSKNLAKRSRKALHYNFKDMGMDWIIFLEYEAFH 328
 DB 315 RRRRTALAGTRAAQSGGAGRGHGRGRSRSKRLHYDFKELGMDWIINADYEAVH 374
 QY 329 CGELCEPPLRSHLEPTNNAVIOTLNSMDPESTPTCCVPTRLSPISILFIDSANNVYK 388
 DB 375 CEGVCDPPLRSHLEPTNNAIOTLNSMAPDAAPASCVPARLSPISILIYIDANNVYK 434
 QY 389 QYEDWVVESSGCR 401
 DB 435 QYEDWVVEAGCR 447

RESULT 9

099MY1 PRELIMINARY; PRT; 441 AA.
 AC 099MY1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Growth/differentiation factor 7 (Fragment).
 GN GDF7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 NC NCBL_Taxid-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TT2;

RX MEDLINE-21136583; PubMed-11238730;
 RA Watahabe A., Fujita H., Hayashi M., Yamamori T.;
 RT "Growth/differentiation factor 7 is preferentially expressed in the
 RT primary motor area of the monkey neocortex."
 RL J. Neurochem. 76:1455-1464(2001).
 CC -1- SIMILARITY: BELONGS TO THE TGF- β FAMILY.
 DR EMBL; AF254571; AAK30843.1; JOINED.
 DR HSSP; P12643; 3BMP.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGF β .
 DR InterPro; IPR001111; TGF β .N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF β -propeptide; 1.
 DR PRINTS; PR00669; INHIBIN.
 DR ProDom; PD000357; TGF β ; 1.
 DR SMART; SM00204; TGF β ; 1.
 DR PROSITE; PS00250; TGF- β 1; 1.
 FT NON_TER
 SQ SEQUENCE 441 AA; 45617 MW; 74DA312A853701F0 CRC64;

Query Match 30.4%; Score 648.5; DB 11; Length 441;

Best Local Similarity 36.8%; Pred. No. 1.3e-47;
Matches 156; Conservative 67; Mismatches 132; Indels 69; Gaps 12;

QY 15 RQATARTVTPKQLPGKAPPKAGVPSSEFLKKAREPGPREPPPTTPHE 71
 DB 30 RAAGAGPVPSPGGGGGGRTLAARA--PGSALGAAVPGRAVRAAGSGFRNGSVPH 86
 QY 72 YMLSYRTLSADRKGNSSVLEA--GLANTITSFIDKG-QDGRPVVRKQRYVEDISA 128
 DB 87 FMSLYRSLA-----GRAPVAAASGHGRVDITGTQATQDETAAREGQSFLEVDSS 140
 QY 129 L-EKDGILGAEILRLKKPSDTAKPAAPGGGAAQ--LKLSCPSGROPASLIDVRSVPGI 187
 DB 141 LSEADEVNAELNVLKRR--SPEDDSATLLPRLILSTCPDEACTAHLHSRAEPIG 197
 QY 188 GSGWEVFDIKLFRNFKN---SAQLCLELEMERGRA--VDLRGIGF-----DRAAQ 235
 DB 198 GARWEAFDVTDAQSHRMWRASRKCIVLATASESPALMRIGFGPGGDDGGTA 257
 QY 236 VHEKALFLVFGRTKRDLEFNEIKANS-----GQDKTYVEYELFQRRKRA 282
 DB 258 AERRALVIVSSRTQKESLFRERIAQARALRAAEPPDPGPGAGSRKANLGRRRRTA 317
 QY 283 PLATR-----QGRKPSKNLAKRSRKALHYNFKDMGMDWIIFLEYEAFH 328
 DB 318 LAGTRGAQSGGGGGGGGGGGGGGGGGGGGGGAGHGRGRSRSKRLHYDFKELGMDWI 377
 QY 318 IIALEYEAFHCEPPLRSHLEPTNNAVIOTLNSMDPESTPTCCVPTRLSPISIL 377
 DB 378 IIAIDYEAVHCGVCDPPLRSHLEPTNNAIOTLNSMAPDAAPASCVPARLSPISIL 437
 QY 378 FIDS 381
 DB 438 YIDA 441

RESULT 10

09W6C0 PRELIMINARY; PRT; 261 AA.
 AC 09W6C0;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Growth/differentiation factor 7 (Fragment).
 GN GDF7.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCBL_Taxid-7955;
 RN [1]


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FT NON_TER 1 1
SQ SEQUENCE 126 AA; 14265 MW; CB824D280F44A394 CRC64;

Query Match
Best Local Similarity 26.6%; Score 567.5; DB 13; Length 126;
Matches 100; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

QY 277 RRRRRAPLATROGKR-PSKNLAKCSRKALHVNFKDGMWDNIAPLEYAEHCEGLCEP 335
DB 1 RRRRRRTTIAARSGRGHGRKAKTRCSKRLPHVNFKELGWDWNIAPLEYAEHCEGCVDF 60

QY 336 PLRSHLEPTNHAIVOTLNMSPDPEPTPCVPTLSPISLIFISANNVYKQYEDMAY 395
DB 61 PLRSHLEPTNHAIVOTLNMSPDPEPTPCVPTLSPISLIFISANNVYKQYEDMAY 120

QY 396 ESCGCR 401
DB 121 ETCGCR 126

RESULT 13
ID 08J1J8 PRELIMINARY; PRT; 403 AA.
AC 08J1J8:
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Bmp4 protein.
GN Bmp4.
OS Haplochromis nyererei.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Haplochromis.
OX NCBI_TaxID=122282;
RN [1]
RP SEQUENCE FROM N.A.
RA Terai Y., Morikawa N., Okada N.;
RT "The evolution of the pro-domain of bone morphogenetic protein 4
RT (Bmp4) in an explosively speciated lineage of East African cichlid
RT fishes.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AB084660; BAC02597.1;
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF000019; TGF-beta.1.
DR PRINTS: PR00688; TGFb-propeptide.1.
DR PRODOM: PD000357; TGFb.1.
DR SMART: SM00204; TGFb.1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
SQ SEQUENCE 403 AA; 46184 MW; 3FA88B37C3988FBC CRC64;

Query Match
Best Local Similarity 21.9%; Score 466.5; DB 13; Length 403;
Matches 130; Conservative 67; Mismatches 132; Indels 91; Gaps 18;

QY 25 KQQLPG--GKAPPKAGSVPSF-----LTKAREGPREPREPPPTIPHEMYSL 76
DB 32 KKKVPELQGRSAQSHELLRDFEATLLHMFGLKRRRPSRSATVP-----RYLDDL 82

QY 77 YRTLSDADRRKGNSSVKLE-----AGLANTITSFIDKQ-----DGRGPVVRKORYE 124
DB 83 YRLQSGEAEAGAHDAIEFYPERASRATVGFHHEEMEDLHELDDGPM--PIRFMF 140

QY 125 DISALEKDGLL-GAEIRIIRKRPSTAKPAAGGGAQK---LSSCPGROPASILD 179
DB 141 NLSSTIPEDLLSSAELRLRHQIDEAIDDAQALHRIINYEVLKAPRQOLITQLD 200

QY 180 VASVPGLDGSGWEVEDI-----WKLFK--NFKNSAQ-LCLELMEKRAVDLRLGFD 230

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DB 201 TRLVRH--NASRSESDVSPAVLWMARERLPNGLAVEVLHLNQTPRHGRHV----- 251
QY 231 RAARQVHE-----KALFLVFGTRKRRDLFEFEIKARSGODDKTYEYELFSORRRR 281
DB 252 RISRSLSHQRPGEWEDLRPLVTFGHDGCHSL-----TRRTKR 290

QY 282 APLATROGKRPSKNLAKCSRKALHVNFKDGMWDNIAPLEYAEHCEGLCEPRLSH 341
DB 291 SP--RQGRKRRNN-----CRRHALYDFSDVGWMDNIAPVQYQAYYCHGCEPFLADHL 344

QY 342 EPTNHAIVOTLNMSPDPEPTPCVPTLSPISLIFISANNVYKQYEDMAYESGCR 401
DB 345 NSTNHAIVOTLVNSVN--NNIPKACVPTLSALSLIDLDEHDKVYLNKQYEMVEGCGCR 403

RESULT 14
ID 08J1J6 PRELIMINARY; PRT; 403 AA.
AC 08J1J6:
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Bmp4 protein.
GN Bmp4.
OS Labidochromis caeruleus (blue streak hap).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Labidochromis.
OX NCBI_TaxID=50897;
RN [1]
RP SEQUENCE FROM N.A.
RA Terai Y., Morikawa N., Okada N.;
RT "The evolution of the pro-domain of bone morphogenetic protein 4
RT (Bmp4) in an explosively speciated lineage of East African cichlid
RT fishes.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AB084662; BAC02599.1;
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF000019; TGF-beta.1.
DR PRINTS: PR00688; TGFb-propeptide.1.
DR PRODOM: PD000357; TGFb.1.
DR SMART: SM00204; TGFb.1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
SQ SEQUENCE 403 AA; 46194 MW; 3E788837C3988C8C CRC64;

Query Match
Best Local Similarity 21.8%; Score 465.5; DB 13; Length 403;
Matches 130; Conservative 67; Mismatches 132; Indels 91; Gaps 18;

QY 25 KQQLPG--GKAPPKAGSVPSF-----LTKAREGPREPREPPPTIPHEMYSL 76
DB 32 KKKVPELQGRSAQSHELLRDFEATLLHMFGLKRRRPSRSATVP-----RYLDDL 82

QY 77 YRTLSDADRRKGNSSVKLE-----AGLANTITSFIDKQ-----DGRGPVVRKORYE 124
DB 83 YRLQSGEAEAGAHDAIEFYPERASRATVGFHHEEMEDLHELDDGPM--PIRFMF 140

QY 125 DISALEKDGLL-GAEIRIIRKRPSTAKPAAGGGAQK---LSSCPGROPASILD 179
DB 141 NLSSTIPEDLLSSAELRLRHQIDEAIDDAQALHRIINYEVLKAPRQOLITQLD 200

QY 180 VASVPGLDGSGWEVEDI-----WKLFK--NFKNSAQ-LCLELMEKRAVDLRLGFD 230
DB 201 TRLVRH--NASRSESDVSPAVLWMARERLPNGLAVEVLHLNQTPRHGRHV----- 251

QY 231 RAARQVHE-----KALFLVFGTRKRRDLFEFEIKARSGODDKTYEYELFSORRRR 281
DB 252 RISRSLSHQRPGEWEDLRPLVTFGHDGCHSL-----TRRTKR 290

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Thu Aug 28 08:27:35 2003

us-09-901-556c-3.rspt

Page 8

[illegible]

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Job time : 104 secs

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AC          OBL19;
DT          01-OCT-2002 (TtEmblrel. 22, Created)
DT          01-OCT-2002 (TtEmblrel. 22, Last sequence update)
DT          01-MAR-2003 (TtEmblrel. 23, Last annotation update)
DE          Bmp4 protein.
GN          Bmp4.
OS          Haplochromis burtoni (Burton's mouthbrooder).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC          Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
OC          Cichlidae; Astotilapia.
OX          NCBI_TaxId=8153;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Tenal Y., Morikawa N., Okada N.;
RT          "The evolution of the pro-domain of bone morphogenetic protein 4
RT          (Bmp4) in an explosively speciated lineage of East African cichlid
RT          fishes."
RL          Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
CC          -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR          EMBL: AB084658; BAC02595.1; -
DR          InterPro: IPR002405; Inhibin_alpha.
DR          InterPro: IPR001839; TGFp.
DR          InterPro: IPR001111; TGFp_N.
DR          Pfam: PR00019; TGF-beta; I.
DR          Pfam: PR00688; TGFp_propeptide; 1.
DR          PRINTS: PR00659; INHIBIN.
DR          ProDom: PD000337; TGFp; 1.
DR          SMART: SM00204; TGFb; 1.
DR          PROSITE: PS00250; TGF_BETA_1; 1.
SQ          SEQUENCE 403 AA; 46196 MW; BD4674F7CF07F854 CRC64;

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Query Match	21.88;	Score 464.5;	DB 13;	Length 403;
Best Local Similarity	32.68;	Pred. No. 8.9e-32;		
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Search completed: August 19, 2003, 10:30:34
Job time : 104 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2003, 10:26:51 ; Search time 30 Seconds

(without alignments)
565.555 Million cell updates/sec

Title: US-09-901-556C-3

Perfect score: 2133
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
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6: /cgn2_6/ptodata/1/1aa/Backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2133	100.0	401	3	US-08-289-222E-3
2	2133	100.0	401	3	US-09-054-526B-1
3	2133	100.0	501	2	US-08-288-508C-2
4	2133	100.0	501	4	US-08-981-450B-1
5	1996	93.6	495	1	US-08-455-559-10
6	1996	93.6	495	5	US-09-145-060-10
7	1996	93.6	495	5	PCT-US94-00657-10
8	771	36.1	321	1	US-08-362-670B-26
9	771	36.1	321	3	US-08-333-576C-26
10	771	36.1	321	3	US-08-808-324-26
11	771	36.1	321	5	PCT-US94-14030A-26
12	658	30.8	120	1	US-08-362-670B-4
13	658	30.8	120	3	US-08-333-576C-4
14	658	30.8	120	3	US-08-808-324-4
15	658	30.8	120	5	PCT-US94-14030A-4
16	658	30.8	388	1	US-08-362-670B-34
17	658	30.8	388	3	US-08-333-576C-34
18	658	30.8	388	5	US-08-808-324-34
19	658	30.8	388	5	PCT-US94-14030A-34
20	655	30.7	263	1	US-08-362-670B-32
21	655	30.7	263	3	US-08-333-576C-32
22	655	30.7	263	3	US-08-808-324-32
23	655	30.7	263	5	PCT-US94-14030A-32
24	649	30.4	119	1	US-08-455-559-13
25	649	30.4	119	5	US-09-145-060-13
26	649	30.4	119	5	PCT-US94-00657-13
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28	606	28.4	294	3	US-08-333-576C-2	Sequence 2, Appl1
29	606	28.4	294	3	US-08-808-324-2	Sequence 2, Appl1
30	606	28.4	294	5	PCT-US94-14030A-2	Sequence 2, Appl1
31	594.5	27.9	411	1	US-08-362-670B-28	Sequence 28, Appl1
32	594.5	27.9	411	3	US-08-333-576C-28	Sequence 28, Appl1
33	594.5	27.9	411	3	US-08-808-324-28	Sequence 28, Appl1
34	594.5	27.9	411	5	PCT-US94-14030A-28	Sequence 28, Appl1
35	573	26.9	134	1	US-08-581-529B-6	Sequence 6, Appl1
36	573	26.9	134	5	US-08-097-616-6	Sequence 6, Appl1
37	573	26.9	134	5	PCT-US94-0762-6	Sequence 6, Appl1
38	568	26.6	102	1	US-08-335-583C-51	Sequence 51, Appl1
39	568	26.6	102	2	US-08-288-508C-13	Sequence 13, Appl1
40	568	26.6	102	3	US-08-289-222E-22	Sequence 22, Appl1
41	568	26.6	102	3	US-09-054-526B-22	Sequence 22, Appl1
42	552	25.9	119	1	US-08-581-529B-7	Sequence 7, Appl1
43	552	25.9	119	5	US-09-097-616-7	Sequence 7, Appl1
44	552	25.9	119	5	PCT-US94-0762-7	Sequence 7, Appl1
45	544	25.5	240	1	US-08-362-670B-30	Sequence 30, Appl1

ALIGNMENTS

RESULT 1
US-08-289-222E-3
Sequence 3, Application US/08289222E
Patent No. 6120760
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289, 222E
FILING DATE: 25-AUG-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289, 222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTIS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 401 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-289-222E-3

Query Match 100.0%; Score 2133; DB 3; Length 401;
 Best Local Similarity 100.0%; Pred. No. 3.4e-186;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGGEPRKPGHPOTROATARTVTPKGLPGKAPPKAGSVSSFLTKKAREPGPREPE 60
 DB 1 PGGEPRKPGHPOTROATARTVTPKGLPGKAPPKAGSVSSFLTKKAREPGPREPE 60
 QY 61 PRPPPTIPHEXMTSLYRTLSADRRKGGSSVYKLEAGLANTTSTFDKGDDRGVYVAKQ 120
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 DB 181 RSVPLDGSQWEVDIKLFRNFKNASQCLLEAMERGRAVDLRLGIGEDRAARQVHEKA 240
 QY 241 LFLVGRTRKKRDLFFNEIKARSGODKTYEYELFSQRRRRAPLATROGKRPSKNTKARC 300
 DB 241 LFLVGRTRKKRDLFFNEIKARSGODKTYEYELFSQRRRRAPLATROGKRPSKNTKARC 300
 QY 301 SRKALHVFNDKMGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHNAYIOTLNSMDPES 360
 DB 301 SRKALHVFNDKMGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHNAYIOTLNSMDPES 360
 QY 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCR 401
 DB 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCR 401

RESULT 2
 US-09-054-526B-3
 Sequence 3, Application US/09054526B
 Patent No. 6197550
 GENERAL INFORMATION:
 APPLICANT: H. TIEN, GERTTRUD
 APPLICANT: NEIDHARDT, HELGE
 APPLICANT: BECHTOLD, ROLF
 APPLICANT: POHL, JENS
 TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP
 STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
 STREET: SUITE 330
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-5701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/054.526B
 FILING DATE: 03-APR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/289,222
 FILING DATE: 12-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 01-JUL-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EPO 92102324.8
 FILING DATE: 12-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/00350
 FILING DATE: 12-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: KITS, MONICA CHIN
 REGISTRATION NUMBER: 36,105
 REFERENCE/DOCKET NUMBER: P564-8005
 TELEPHONE: 202/638-5000
 TELEFAX: 202/638-4810
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 401 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-054-526B-3

Query Match 100.0%; Score 2133; DB 3; Length 401;
 Best Local Similarity 100.0%; Pred. No. 3.4e-186;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGGEPRKPGHPOTROATARTVTPKGLPGKAPPKAGSVSSFLTKKAREPGPREPE 60
 DB 1 PGGEPRKPGHPOTROATARTVTPKGLPGKAPPKAGSVSSFLTKKAREPGPREPE 60
 QY 61 PRPPPTIPHEXMTSLYRTLSADRRKGGSSVYKLEAGLANTTSTFDKGDDRGVYVAKQ 120
 DB 61 PRPPPTIPHEXMTSLYRTLSADRRKGGSSVYKLEAGLANTTSTFDKGDDRGVYVAKQ 120
 QY 121 RYVEDISALEKDLGAEIRLIRKRPSTAKPAAGGGRAGAAQLKSSCPGROPASLIDY 180
 DB 121 RYVEDISALEKDLGAEIRLIRKRPSTAKPAAGGGRAGAAQLKSSCPGROPASLIDY 180
 QY 181 RSVPLDGSQWEVDIKLFRNFKNASQCLLEAMERGRAVDLRLGIGEDRAARQVHEKA 240
 DB 181 RSVPLDGSQWEVDIKLFRNFKNASQCLLEAMERGRAVDLRLGIGEDRAARQVHEKA 240
 QY 241 LFLVGRTRKKRDLFFNEIKARSGODKTYEYELFSQRRRRAPLATROGKRPSKNTKARC 300
 DB 241 LFLVGRTRKKRDLFFNEIKARSGODKTYEYELFSQRRRRAPLATROGKRPSKNTKARC 300
 QY 301 SRKALHVFNDKMGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHNAYIOTLNSMDPES 360
 DB 301 SRKALHVFNDKMGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHNAYIOTLNSMDPES 360
 QY 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCR 401
 DB 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVESGCR 401

RESULT 3
 US-08-288-508C-2
 Sequence 2, Application US/08288508C
 Patent No. 5994094
 GENERAL INFORMATION:
 APPLICANT: H. TIEN, GERTTRUD
 APPLICANT: NEIDHARDT, HELGE
 APPLICANT: PAULISTA, MICHAEL
 TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP
 STREET: 655 FIFTEENTH STREET N.W. Suite 330
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.

```

; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,508C
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 26 829.3
; FILING DATE: 10-AUG-1993
; APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 18 222.8
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 20 157.5
; FILING DATE: 09-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JAHNS, Kristina M.
; REGISTRATION NUMBER: P-41,092
; REFERENCE/DOCKET NUMBER: P564-4019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-288-508C-2

```

Query Match 100.0%; Score 2133; DB 2; Length 501;

Best Local Similarity 100.0%; Pred. No. 4,6e-186; Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PGSPRPKGNHPPQTRQATARTVTPKGLPGKAPKAGSVSPSSFLTKKAREGPPREPKE 60
DB 101 PGSPRPKGNHPPQTRQATARTVTPKGLPGKAPKAGSVSPSSFLTKKAREGPPREPKE 160
QY 61 PRRPPPTIRPHEYMLSLYRTLSDADRRKGNSSVYLEAGLANITTSFTDKQDDRGVVRKQ 120
DB 161 PRRPPPTIRPHEYMLSLYRTLSDADRRKGNSSVYLEAGLANITTSFTDKQDDRGVVRKQ 220
QY 121 RYVFDSALEKDKGLGAEELRIIRKRPSPDAPKAPAGGGRAAOLKLSGCGSPGQPSLIDY 180
DB 221 RYVFDSALEKDKGLGAEELRIIRKRPSPDAPKAPAGGGRAAOLKLSGCGSPGQPSLIDY 280
QY 181 RSVPGIDSGGWEVFIDWIKLFERNFKNSAQLCLELAEAMERGRAVDLGLGFDRARAQVHEKA 240
DB 281 RSVPGIDSGGWEVFIDWIKLFERNFKNSAQLCLELAEAMERGRAVDLGLGFDRARAQVHEKA 340
QY 241 LFLVFGRTKKRDLFENEIKANSQDDKTYEYLFESQRRRRAPLATROGKRPSKMLKARC 300
DB 341 LFLVFGRTKKRDLFENEIKANSQDDKTYEYLFESQRRRRAPLATROGKRPSKMLKARC 400
QY 301 SRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAAYIOTLMSNDPES 360
DB 401 SRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAAYIOTLMSNDPES 460
QY 361 TPPTCCVPTRLSPISITLFDISANNVYKQEDMVVESCGR 401
DB 461 TPPTCCVPTRLSPISITLFDISANNVYKQEDMVVESCGR 501

```

RESULT 4
US-08-981-490B-1
; Sequence 1, Application US/08981490B
; Patent No. 6531450
; GENERAL INFORMATION:
; APPLICANT: Hotten, Gertrud

```

; APPLICANT: Pohl, Jens
; APPLICANT: Bechtold, Rolf
; APPLICANT: Paulista, Michael
; APPLICANT: Unsicker, Klaus
; TITLE OF INVENTION: USE OF MP2 OR MP121 FOR TREATING AND PREVENTING DISEASES OF T
; TITLE OF INVENTION: NERVOUS SYSTEM
; FILE REFERENCE: 100564-07032
; CURRENT APPLICATION NUMBER: US/08/981,490B
; CURRENT FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DE/195 25 416.3
; PRIOR FILING DATE: 1995-07-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-981-490B-1

```

Query Match 100.0%; Score 2133; DB 4; Length 501;

Best Local Similarity 100.0%; Pred. No. 4,6e-186; Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PGSPRPKGNHPPQTRQATARTVTPKGLPGKAPKAGSVSPSSFLTKKAREGPPREPKE 60
DB 101 PGSPRPKGNHPPQTRQATARTVTPKGLPGKAPKAGSVSPSSFLTKKAREGPPREPKE 160
QY 61 PRRPPPTIRPHEYMLSLYRTLSDADRRKGNSSVYLEAGLANITTSFTDKQDDRGVVRKQ 120
DB 161 PRRPPPTIRPHEYMLSLYRTLSDADRRKGNSSVYLEAGLANITTSFTDKQDDRGVVRKQ 220
QY 121 RYVFDSALEKDKGLGAEELRIIRKRPSPDAPKAPAGGGRAAOLKLSGCGSPGQPSLIDY 180
DB 221 RYVFDSALEKDKGLGAEELRIIRKRPSPDAPKAPAGGGRAAOLKLSGCGSPGQPSLIDY 280
QY 181 RSVPGIDSGGWEVFIDWIKLFERNFKNSAQLCLELAEAMERGRAVDLGLGFDRARAQVHEKA 240
DB 281 RSVPGIDSGGWEVFIDWIKLFERNFKNSAQLCLELAEAMERGRAVDLGLGFDRARAQVHEKA 340
QY 241 LFLVFGRTKKRDLFENEIKANSQDDKTYEYLFESQRRRRAPLATROGKRPSKMLKARC 300
DB 341 LFLVFGRTKKRDLFENEIKANSQDDKTYEYLFESQRRRRAPLATROGKRPSKMLKARC 400
QY 301 SRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAAYIOTLMSNDPES 360
DB 401 SRKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAAYIOTLMSNDPES 460
QY 361 TPPTCCVPTRLSPISITLFDISANNVYKQEDMVVESCGR 401
DB 461 TPPTCCVPTRLSPISITLFDISANNVYKQEDMVVESCGR 501

```

RESULT 5
US-08-455-559-10
; Sequence 10, Application US/08455559
; Patent No. 5801014
; GENERAL INFORMATION:
; APPLICANT: LEE, SE-JIN
; APPLICANT: HOYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-559-10

```

```

Query Match          93.6%; Score 1996; DB 1; Length 495;
Best Local Similarity 94.5%; Pred. No. 1.3e-173;
Matches 378; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

```

```

QY 2 GPEPKGHPQOTQATRTVTPKQLPFGKAPKAGSVSSFLTKKAREGPPREPEK 61
DB 96 GSETRKGPSSQFOAARVTPKQLPFGKASKAGSAPSSFLTKKREGTREPEK 155
QY 62 FRPPITPHEMYSLYRTSLDADKGNSSVYLEAGLANTITSFIDKQDDRGPAVRKOR 121
DB 156 FRPPITPHEMYSLYRTSLDADKGNSSVYLEAGLANTITSFIDKQDDRGPAVRKOR 215
QY 122 YVFDISALEKDGILGAEIRILRRKPSDPAKPAAGGGAOLKISCPGSGROPASLLDVR 181
DB 216 YVFDISALEKDGILGAEIRILRRKPSDPAKPAAGGGAOLKISCPGSGROPASLLDVR 275
QY 182 SVPLDGSQGEVVDIMKLFNFNFKNSAOLCLELAWERGRAVDLGLGFERRAQRVHEKAL 241
DB 276 SVPLDGSQGEVVDIMKLFNFNFKNSAOLCLELAWERGRAVDLGLGFERRAQRVHEKAL 335
QY 242 FLVFGRTKKRDLFNEIKARSGODKTYEYLFSGRRRAPLATTROGKRPSKILKARCS 301
DB 336 FLVFGRTKKRDLFNEIKARSGODKTYEYLFSGRRRAPLATTROGKRPSKILKARCS 395
QY 302 RKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHAVIOTLANSMDPEST 361
DB 396 RKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHAVIOTLANSMDPEST 455
QY 362 PPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 401
DB 456 PPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 495

```

```

RESULT 6
US-09-145-060-10
Sequence 10, Application US/09145060
Patent No. 6245896
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haller, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-09-145-060-10

```

```

Query Match          93.6%; Score 1996; DB 3; Length 495;
Best Local Similarity 94.5%; Pred. No. 1.3e-173;
Matches 378; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

```

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QY 2 GPEPKGHPQOTQATRTVTPKQLPFGKAPKAGSVSSFLTKKAREGPPREPEK 61
DB 96 GSETRKGPSSQFOAARVTPKQLPFGKASKAGSAPSSFLTKKREGTREPEK 155
QY 62 FRPPITPHEMYSLYRTSLDADKGNSSVYLEAGLANTITSFIDKQDDRGPAVRKOR 121
DB 156 FRPPITPHEMYSLYRTSLDADKGNSSVYLEAGLANTITSFIDKQDDRGPAVRKOR 215
QY 122 YVFDISALEKDGILGAEIRILRRKPSDPAKPAAGGGAOLKISCPGSGROPASLLDVR 181
DB 216 YVFDISALEKDGILGAEIRILRRKPSDPAKPAAGGGAOLKISCPGSGROPASLLDVR 275
QY 182 SVPLDGSQGEVVDIMKLFNFNFKNSAOLCLELAWERGRAVDLGLGFERRAQRVHEKAL 241
DB 276 SVPLDGSQGEVVDIMKLFNFNFKNSAOLCLELAWERGRAVDLGLGFERRAQRVHEKAL 335
QY 242 FLVFGRTKKRDLFNEIKARSGODKTYEYLFSGRRRAPLATTROGKRPSKILKARCS 301
DB 336 FLVFGRTKKRDLFNEIKARSGODKTYEYLFSGRRRAPLATTROGKRPSKILKARCS 395
QY 302 RKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHAVIOTLANSMDPEST 361
DB 396 RKALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPLRSHLEPTNHAVIOTLANSMDPEST 455
QY 362 PPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 401
DB 456 PPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 495

```

```

RESULT 7
PCT-US94-00657-10
Sequence 10, Application PC/TUS9400657
GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
APPLICANT: HOYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LOBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR

```

CITY: LOS ANGELES
 STATE: CALIFORNIA
 COUNTRY: US
 ZIP: 90067
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/00657
 FILING DATE: 1/12/94
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: WETHERELL, JR. PH.D., JOHN R.
 REGISTRATION NUMBER: 31,678
 REFERENCE/DOCKET NUMBER: PD3256 CIP OF PD2280
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/455-5100
 TELEFAX: 619-455-5110
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 495 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US94-00657-10

Query Match 93.6%; Score 1996; DB 5; Length 495;
 Best Local Similarity 94.5%; Pred. No. 1.3e-173;
 Matches 378; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

2 GPEPRKPPHPOTROATATATVTPKGLPGKAPKAGSVSSFLKKAREPPPREPEP 61
 96 GSEKRPSPSOTRRAAARTYTPKQLPGKASAGAPSPSFLKKTREPTPREPEP 155
 62 FRPPPTHEHYMLSYRTLSADRRKGNSSVYLEAGLANTTSFTDKGODDGPVYROR 121
 156 FRPPPTHEHYMLSYRTLSADRRKGNSSVYLEAGLANTTSFTDKGODDGPVYROR 215
 122 YVFDLSALEKDGILGAEIRILRKRPSPDAKPAAPGGGAAOLKLSGSGRQPAALLDVR 181
 216 YVFDLSALEKDGILGAEIRILRKRPSPDAKPAAPGGGAAOLKLSGSGRQPAALLDVR 275
 182 SVPGIDSGMEVFDMWKLEFRNFKNSAQCLLEAERGRAVDLRGLGFDRARAQYHEKAL 241
 276 SVPGIDSGMEVFDMWKLEFRNFKNSAQCLLEAERGRAVDLRGLGFDRARAQYHEKAL 335
 242 FLVFGRTKRRDLFENEIRARSGODDKTYEYLFSGRRRRAPLATRQGRPSKRLKARCS 301
 336 FLVFGRTKRRDLFENEIRARSGODDKTYEYLFSGRRRRAPLATRQGRPSKRLKARCS 395
 302 RKALHVNFKDMGMDWMIAPLEYEAFHCEPLRSHLEPTNNAVITQTLNMSMDPEST 361
 336 RKALHVNFKDMGMDWMIAPLEYEAFHCEPLRSHLEPTNNAVITQTLNMSMDPEST 455
 362 PPTCCVPTRLSPISILFTDSANNVYVKQYEDMVVSCGCR 401
 456 PPTCCVPTRLSPISILFTDSANNVYVKQYEDMVVSCGCR 495

RESULT 8

US-08-362-670B-26
 Sequence 26, Application US/08362670B
 Patent No. 5658882

GENERAL INFORMATION:

APPLICANT: Celeste, Anthony J.
 APPLICANT: Mooney, John
 APPLICANT: Rosen, Vicki A.
 APPLICANT: Wolfman, Neil
 APPLICANT: Thomsen, Gerald H.
 APPLICANT: Melton, Douglas A.
 TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/362,670B
 FILING DATE: December 22, 1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REGISTRATION NUMBER: 32,618
 REFERENCE/DOCKET NUMBER: 5202-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498-8260
 TELEFAX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-362-670B-26

Query Match 36.1%; Score 771; DB 1; Length 321;
 Best Local Similarity 51.1%; Pred. No. 2.8e-62;
 Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

117 VRKQRYVFDISAL-EKDGILGAEIRILRKRPSPDAKPAAPGGGAAOL-KLSGSGRQ 173
 9 LRQRYLFDVSLSKELVGAELRLFGAPG-----APGPPAGPLHYQFLPGLS--- 59
 174 PASLIDVNSV--PGIDSGMEVFDMWKLEFRNFKNSAQCLLEA-AM---ERGRA----- 221
 60 -PLLDARTLDPDQGAAPPAGMEVFDMWQGLRH-QPKQICLLEIRAAWGELDAGEAARARG 117
 222 -----VDLRGFGFRARAQYHEKALFLVFGRTKRRDLFENEIRARSGODDKT----- 268
 118 PQQPPPTRLSGIFGRRRRPPQERALLVFTSRKRL-FAERQQLSAAEAGPAGAE 176
 269 -----VYELFSG-RRKRRAPLATRQGRPSKRLKARCSRKALHVNFKDMGMD 316
 177 GSWPPSGADPARPMLPSPGRRRRTAFASRRGRKRRKSKRLPLHVNFKELGMD 236
 317 WIAALEYEAFCDELCFPLRSHLEPTNNAVITQTLNMSMDPESTPPTCCVPTRLSPISI 376
 237 WIAALEYEAFCDELCFPLRSHLEPTNNAVITQTLNMSMDPGSTPPSCVPTKLTPLSI 296
 377 LFTDSANNVYVKQYEDMVVSCGCR 401
 297 LYIDAGNNVYVKQYEDMVVSCGCR 321

RESULT 9

US-08-333-576C-26
 Sequence 26, Application US/08333576C
 Patent No. 6027919

GENERAL INFORMATION:

APPLICANT: Celeste, Anthony J.
 APPLICANT: Mooney, John
 APPLICANT: Rosen, Vicki A.
 APPLICANT: Wolfman, Neil
 APPLICANT: Thomsen, Gerald H.
 APPLICANT: Melton, Douglas A.
 TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,576C
FILING DATE: No. 6027919ember 2, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-576C-26

Query Match 36.1%, Score 771; DB 3; Length 321;
Best Local Similarity 51.1%, Pred. No. 2,8e-62;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

117 VRKQYVYDISAL-EKDLGLGAEELRLKRPSTAKPAAGGGAOL--KLSCPSGRQ 173
DB 9 LRQKLYFDVMSLDEKELVGAELRLFRQAPS-----APGPPAGLHVQLFCLSL 59
QY 174 PASLIDVRSV--PGIDSGMEVEDIKLFENFKNSAOLCLEL-AM--EGRRA----- 221
DB 60 -PLILDATLDPQAGPPAGMEVFVWQGLRH-QPWKOLCUELRAMWELDAGEAEARARG 117
QY 222 -----VDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFENEIKARSGODDKT----- 268
DB 118 PQQPPPLRLSLGGRVRRPQERALLVFTRSQKRL-FAEMREQLGSAAAGPGAGAE 176
QY 269 -----VYEYLFQ--RRKRRAPLATROGKRPSKNTKARCSRKALHVNFKDMGMD 316
DB 177 GSWPPSGAPDARPMLPSGRRRRRTAFASRHGKRKSRRLRCSKPLHVNFKELGMD 236
QY 317 WIIAPLEYAEAFHCGELCEPRLSHLEPTNNAVITOTLNMSMDPESTPPTCCVPTRLSPISI 376
DB 237 WIIAPLEYAEAFHCGVCDPFLRSLHLEPTNNAVITOTLNMSMDPGSTPPSCVPTKLTPTISI 296
QY 377 LFIDSANNVYKQYEDMAYVESCGR 401
DB 297 LYIDAGNNVYKQYEDMAYVESCGR 321

RESULT 10
US-08-808-324-26
Sequence 26, Application US/08808324
Patent No. 6284872
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Mooney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-808-324-26

Query Match 36.1%, Score 771; DB 3; Length 321;
Best Local Similarity 51.1%, Pred. No. 2,8e-62;
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

117 VRKQYVYDISAL-EKDLGLGAEELRLKRPSTAKPAAGGGAOL--KLSCPSGRQ 173
DB 9 LRQKLYFDVMSLDEKELVGAELRLFRQAPS-----APGPPAGLHVQLFCLSL 59
QY 174 PASLIDVRSV--PGIDSGMEVEDIKLFENFKNSAOLCLEL-AM--EGRRA----- 221
DB 60 -PLILDATLDPQAGPPAGMEVFVWQGLRH-QPWKOLCUELRAMWELDAGEAEARARG 117
QY 222 -----VDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFENEIKARSGODDKT----- 268
DB 118 PQQPPPLRLSLGGRVRRPQERALLVFTRSQKRL-FAEMREQLGSAAAGPGAGAE 176
QY 269 -----VYEYLFQ--RRKRRAPLATROGKRPSKNTKARCSRKALHVNFKDMGMD 316
DB 177 GSWPPSGAPDARPMLPSGRRRRRTAFASRHGKRKSRRLRCSKPLHVNFKELGMD 236
QY 317 WIIAPLEYAEAFHCGELCEPRLSHLEPTNNAVITOTLNMSMDPESTPPTCCVPTRLSPISI 376
DB 237 WIIAPLEYAEAFHCGVCDPFLRSLHLEPTNNAVITOTLNMSMDPGSTPPSCVPTKLTPTISI 296
QY 377 LFIDSANNVYKQYEDMAYVESCGR 401
DB 297 LYIDAGNNVYKQYEDMAYVESCGR 321

RESULT 11
PCT-US94-14030A-26
Sequence 26, Application PC/TUS9414030A
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge

Query Match	36.1%;	Score 771;	DB 5;	Length 321;
Best Local Similarity	51.1%;	Pred. No. 2.8e-62;		
Matches 166;	Conservative 46;	Mismatches 61;	Indels 52;	Gaps 12

RESULT 12
US-08-362-670B-4
: Sequence 4, Application US/08362670B
: Patent No. 5658862

Query Match	30.8%	Score 658	DB 1	Length 120
Best Local Similarity	100.0%	Pred. No.	1.5e-52	
Matches 120; Conservative	0;	Mismatches	0;	Gaps 0

RESULT 13
US-08-333-576C-4

GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Woliman, Neil
APPLICANT: Thomson, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/333,576C
FILING DATE: No. 6027919ember 2, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-576C-4

Query Match 30.8%; Score 658; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 APLATROGKRPSSKNLKACSRKALHVNFRDGMWDWIIAPLEYEAFHCEGLCEPPLRSHL 341
DB 1 APLATROGKRPSSKNLKACSRKALHVNFRDGMWDWIIAPLEYEAFHCEGLCEPPLRSHL 60
QY 342 EPTNHAIVOTLMSNDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVYESGCR 401
DB 61 EPTNHAIVOTLMSNDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVYESGCR 120

RESULT 14
US-08-808-324-4
Sequence 4, Application US/08808324
Patent No. 6284872
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Yacki A.
APPLICANT: Molman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-808-324-4
Query Match 30.8%; Score 658; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US94-14030A-4
Sequence 4, Application PC/TUS9414030A
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202D-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14030A-4

Query Match 30.8%; Score 658; DB 5; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 APLATROGKRPSSKNLKACSRKALHVNFRDGMWDWIIAPLEYEAFHCEGLCEPPLRSHL 341
DB 1 APLATROGKRPSSKNLKACSRKALHVNFRDGMWDWIIAPLEYEAFHCEGLCEPPLRSHL 60
QY 342 EPTNHAIVOTLMSNDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVYESGCR 401
DB 61 EPTNHAIVOTLMSNDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVYESGCR 120

Thu Aug 28 08:27:33 2003

us-09-901-556c-3.rai

Page 9

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Job time : 31 secs

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GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: August 19, 2003, 10:28:21 ; Search time 27 Seconds

(without alignments)
1945.641 Million cell updates/sec

Title: US-09-901-556c-3

Perfect score: 2133
Sequence: 1 PGGEPRKGPHTQATATAR.....ANNVYKQYEDMAYESGCCR 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2133	100.0	501	8 US-08-981-490B-1	Sequence 1, Appl1
2	2094	98.2	502	10 US-09-813-398-37	Sequence 37, Appl1
3	2075	97.3	501	9 US-09-730-772-13	Sequence 13, Appl1
4	2075	97.3	501	9 US-09-735-849-13	Sequence 13, Appl1
5	1996	93.6	495	10 US-09-880-708-10	Sequence 10, Appl1
6	903	42.3	436	9 US-09-730-772-14	Sequence 14, Appl1
7	903	42.3	436	9 US-09-735-849-14	Sequence 14, Appl1
8	771	36.1	321	10 US-09-945-182-26	Sequence 26, Appl1
9	752.5	35.3	450	15 US-10-188-246-12	Sequence 26, Appl1
10	658	30.8	120	10 US-09-945-182-4	Sequence 4, Appl1
11	658	30.8	388	10 US-09-945-182-34	Sequence 34, Appl1
12	655	30.7	263	10 US-09-945-182-32	Sequence 32, Appl1
13	654	30.7	119	8 US-08-945-459A-1	Sequence 1, Appl1
14	654	30.7	119	10 US-09-068-253-2	Sequence 2, Appl1
15	649	30.4	119	10 US-09-880-708-13	Sequence 13, Appl1

16	606	28.4	294	10 US-09-945-182-2	Sequence 2, Appl1
17	594.5	27.9	411	10 US-09-945-182-28	Sequence 28, Appl1
18	544	25.5	240	10 US-09-945-182-30	Sequence 30, Appl1
19	443	20.8	396	8 US-08-957-425-5	Sequence 5, Appl1
20	440	20.6	396	8 US-09-957-360-2	Sequence 2, Appl1
21	440	20.6	396	11 US-09-804-625-4	Sequence 4, Appl1
22	440	20.6	396	12 US-10-139-814-2	Sequence 2, Appl1
23	440	20.6	396	12 US-10-286-152A-2	Sequence 2, Appl1
24	440	20.6	396	14 US-10-044-716-2	Sequence 0, Appl1
25	440	20.6	396	15 US-10-122-026-10	Sequence 24, Appl1
26	440	20.6	397	10 US-09-813-398-24	Sequence 19, Appl1
27	435	20.4	419	8 US-08-957-425-19	Sequence 69, Appl1
28	426	20.0	408	10 US-09-749-728B-69	Sequence 18, Appl1
29	426	20.0	408	12 US-10-139-814-18	Sequence 4, Appl1
30	426	20.0	408	12 US-10-286-152A-4	Sequence 27, Appl1
31	426	20.0	409	10 US-09-813-398-27	Sequence 7, Appl1
32	423	19.8	408	8 US-08-957-425-7	Sequence 6, Appl1
33	423	19.8	408	11 US-09-804-625-6	Sequence 21, Appl1
34	423	19.8	408	15 US-10-122-026-11	Sequence 31, Appl1
35	421.5	19.8	419	9 US-09-784-911-2	Sequence 12, Appl1
36	421	19.7	453	15 US-10-122-026-18	Sequence 29, Appl1
37	420.5	19.7	454	12 US-10-286-152A-6	Sequence 21, Appl1
38	420.5	19.7	455	10 US-09-813-398-28	Sequence 28, Appl1
39	417.5	19.6	427	9 US-09-784-911-6	Sequence 6, Appl1
40	414	19.4	402	15 US-10-050-050-21	Sequence 21, Appl1
41	414	19.4	403	9 US-09-813-398-31	Sequence 4, Appl1
42	412.5	19.3	437	9 US-09-784-911-4	Sequence 12, Appl1
43	411.5	19.3	588	15 US-10-122-026-12	Sequence 29, Appl1
44	410	19.2	402	8 US-08-957-425-29	Sequence 21, Appl1
45	410	19.2	402	8 US-08-260-675-21	

ALIGNMENTS

```

RESULT 1
US-08-981-490B-1
; Sequence 1, Application US/08981490B
; Publication No. US20020045568A1
GENERAL INFORMATION:
; APPLICANT: Hottel, Gertrud
; APPLICANT: Pohl, Jens
; APPLICANT: Bechtold, Rolf
; APPLICANT: Paulista, Michael
; APPLICANT: Unsicker, Klaus
; TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF T
; TITLE OF INVENTION: NERVOUS SYSTEM
; FILE REFERENCE: 100564-07032
; CURRENT APPLICATION NUMBER: US/08/981,490B
; CURRENT FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: PCT/EP96/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DE/195 25 416.3
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-981-490B-1
Query Match      100.0%  Score 2133; DB 8; Length 501;
Best Local Similarity 100.0%; Pred. No. 5.9e-167;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PGGEPRKGPHTQATATATYTPKGQLPGGKAPPKAGSVSSFLTKKAREGPPREPK 60
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DB 101 PGGEPRKGPHTQATATATYTPKGQLPGGKAPPKAGSVSSFLTKKAREGPPREPK 160
    |||||
QY 61 PRRPPTTPHEHMLSLYRTLSADAKKGGNSVYLEAGLANTTSTIDKGGDDRGVVRKQ 120
    |||||
DB 161 PRRPPTTPHEHMLSLYRTLSADAKKGGNSVYLEAGLANTTSTIDKGGDDRGVVRKQ 220
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Page 2

QY 121 RYVEDISALEKDGILGAEILRIIRKPSDTAKPAAPGGRAAQLKISSCPSGROPASILDV 180
DB 221 RYVEDISALEKDGILGAEILRIIRKPSDTAKPAAPGGRAAQLKISSCPSGROPASILDV 280
QY 181 RSVPGIDSGWEVDIWKLFNFKNKSAQLCLELWEMERGAVDLRGLGFDRAAQAQVHEKA 240
DB 281 RSVPGIDSGWEVDIWKLFNFKNKSAQLCLELWEMERGAVDLRGLGFDRAAQAQVHEKA 340
QY 241 LEIVGRTKKRDLFFNEIKARSGODDKTYEYLFSSORRRAPAPLATROGRPSKNTLARC 300
DB 341 LEIVGRTKKRDLFFNEIKARSGODDKTYEYLFSSORRRAPAPLATROGRPSKNTLARC 400
QY 301 SRKALHYAFKMGMDWITAPLEYEAFHCBGLCEPPLRSHLEPTNNAVIOTLANSMDPS 360
DB 401 SRKALHYAFKMGMDWITAPLEYEAFHCBGLCEPPLRSHLEPTNNAVIOTLANSMDPS 460
QY 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMAYVESGCR 401
DB 461 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMAYVESGCR 501

RESULT 2
US-09-813-398-37
Sequence 37, Application US/09813398
Patent No. US20020169292A1
GENERAL INFORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Szkudlinski
TITLE OF INVENTION: CYSTEINE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: USFMD.00301
CURRENT APPLICATION NUMBER: US/09/813.398
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/US98/19772
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 37
LENGTH: 502
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-09-813-398-37

Query Match 98.2%; Score 2094; DB 10; Length 502;
Best Local Similarity 98.3%; Pred. No. 9.4e-164;
Matches 394; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 RSGPEPKRGPHTROTATARTVTPTKQGLPGKAPPKAGSVSSFLTKKAREPGPREPKE 60
DB 102 RSGPEPKRGPHTROTATARTVTPTKQGLPGKAPPKAGSVSSFLTKKAREPGPREPKE 161
QY 61 PPRPPPTTHHEMYMLSLYRTLSADARKGNSSVKLEAGLANITTSFIDKGODDRGPVVRKQ 120
DB 162 PPRPPPTTHHEMYMLSLYRTLSADARKGNSSVKLEAGLANITTSFIDKGODDRGPVVRKQ 221
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DB 222 RYVEDISALEKDGILGAEILRIIRKPSDTAKPAAPGGRAAQLKISSCPSGROPASILDV 281
QY 181 RSVPGIDSGWEVDIWKLFNFKNKSAQLCLELWEMERGAVDLRGLGFDRAAQAQVHEKA 240
DB 282 RSVPGIDSGWEVDIWKLFNFKNKSAQLCLELWEMERGAVDLRGLGFDRAAQAQVHEKA 341
QY 241 LEIVGRTKKRDLFFNEIKARSGODDKTYEYLFSSORRRAPAPLATROGRPSKNTLARC 300
DB 342 LEIVGRTKKRDLFFNEIKARSGODDKTYEYLFSSORRRAPAPLATROGRPSKNTLARC 401
QY 301 SRKALHYAFKMGMDWITAPLEYEAFHCBGLCEPPLRSHLEPTNNAVIOTLANSMDPS 360
DB 402 SRKALHYAFKMGMDWITAPLEYEAFHCBGLCEPPLRSHLEPTNNAVIOTLANSMDPS 461

QY 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMAYVESGCR 401
DB 462 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMAYVESGCR 502

RESULT 3
US-09-730-772-13
Sequence 13, Application US/09730772
Patent No. US20010011131A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knodde, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730.772
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,081
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfield, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-730-772-13

Query Match 97.3%; Score 2075; DB 9; Length 501;
Best Local Similarity 97.8%; Pred. No. 3.4e-162;
Matches 392; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 1 RSGPEPKRGPHTROTATARTVTPTKQGLPGKAPPKAGSVSSFLTKKAREPGPREPKE 60
DB 101 RSGPEPKRGPHTROTATARTVTPTKQGLPGKAPPKAGSVSSFLTKKAREPGPREPKE 160
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DB 161 PPRPPPTTHHEMYMLSLYRTLSADARKGNSSVKLEAGLANITTSFIDKGODDRGPVVRKQ 220
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DB 222 RYVEDISALEKDGILGAEILRIIRKPSDTAKPAAPGGRAAQLKISSCPSGROPASILDV 280
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DB 281 RSVPGIDSGWEVDIWKLFNFKNKSAQLCLELWEMERGAVDLRGLGFDRAAQAQVHEKA 340

QY 241 LFLVGRTRKRLDFENEIKARSGODKTYEYLFSGRRRRAPLATROCKRRPSKNIKARC 300
 DB 341 LFLVGRTRKRLDFENEIKARSGODKTYEYLFSGRRRRAPLATROCKRRPSKNIKARC 400
 QY 301 SRKALHVNFKDGMWDWIIAPLEYEAFHCEGLCEPFLRSHLEPTNNAVYQTLMSNDPES 360
 DB 401 SRKALHVNFKDGMWDWIIAPLEYEAFHCEGLCEPFLRSHLEPTNNAVYQTLMSNDPES 460
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 DB 461 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGR 501
 RESULT 4
 US-09-735-849-13
 ; Sequence 13, Application US/09735849
 ; Patent No. US20010037017A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Luyten, Frank P.
 ; APPLICANT: Moos, Jr., Malcolm
 ; APPLICANT: Chang, Steven Chao-Huan
 ; TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
 ; TITLE OF INVENTION: PROTEINS
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson & Bear
 ; STREET: 620 Newport Center Drive, 16th Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FASTSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/735.849
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/836,081
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bartfeld, Neil S
 ; REGISTRATION NUMBER: 39,901
 ; REFERENCE/DOCKET NUMBER: NIH099.001APC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-235-8550
 ; TELEFAX: 619-235-0176
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 501 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-735-849-13
 Query Match 97.3%; Score 2075; DB 9; Length 501;
 Best Local Similarity 97.8%; Pred. No. 3.4e-162;
 Matches 392; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 1 PGCPPEKPGHPROTQATARTVTPKGLPGKAPPGAGVSPSFLTKKAREPPREPRE 60
 DB 101 PGCPPEKPGHPROTQATARTVTPKGLPGKAPPGAGVSPSFLTKKAREPPREPRE 160
 QY 61 PRPPPTTPHEHMLSLYRTLSDADRGKSSVYKLEAGLANITTSFIDKSGDDRGVYVRRQ 120
 DB 161 PRPPPTTPHEHMLSLYRTLSDADRGKSSVYKLEAGLANITTSFIDKSGDDRGVYVRRQ 220
 QY 121 RYVFDISALEKDGILGAEILRIIRKKRPSTAKPAAPGGGAAOLKISSCPSGHQPSALDV 180

DB 221 RYVFDISALEKDGILGAEILRIIRKKRPSTAKPAAPGGGAAOLKISSCPSGHQPSALDV 280
 QY 181 RSVPGDLSGMEWFDIWKLFERNFKNSAQCLELEAERGRAVDLGLGDRAROVHEKA 240
 DB 281 RSVPGDLSGMEWFDIWKLFERNFKNSAQCLELEAERGRAVDLGLGDRAROVHEKA 340
 QY 241 LFLVGRTRKRLDFENEIKARSGODKTYEYLFSGRRRRAPLATROCKRRPSKNIKARC 300
 DB 341 LFLVGRTRKRLDFENEIKARSGODKTYEYLFSGRRRRAPLATROCKRRPSKNIKARC 400
 QY 301 SRKALHVNFKDGMWDWIIAPLEYEAFHCEGLCEPFLRSHLEPTNNAVYQTLMSNDPES 360
 DB 401 SRKALHVNFKDGMWDWIIAPLEYEAFHCEGLCEPFLRSHLEPTNNAVYQTLMSNDPES 460
 QY 361 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGR 401
 DB 461 TPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVSCGR 501
 RESULT 5
 US-09-880-708-10
 ; Sequence 10, Application US/09880708
 ; Patent No. US20020165361A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, Se-jin
 ; APPLICANT: Huynh, Thanh
 ; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
 ; STREET: 4365 Executive Drive, Suite 1600
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92121-2189
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/880,708
 ; FILING DATE: 12-Jun-2001
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/145,060
 ; FILING DATE: <unknown>
 ; APPLICATION NUMBER: 08/003,144
 ; FILING DATE: 12-Jan-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lisa A. Halle, Ph.D.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07265/057002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 858/677-1456
 ; TELEFAX: 619/677-1465
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 495 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 ; US-09-880-708-10
 Query Match 93.6%; Score 1996; DB 10; Length 495;
 Best Local Similarity 94.5%; Pred. No. 1e-155;
 Matches 378; Conservative 2; Mismatches 20; Indels 0; Gaps 0;
 QY 2 GGSEPRGHPROTQATARTVTPKGLPGKAPPRKAGVSPSFLTKKAREPPREPRE 61
 DB 96 GGSEPRGHPROTQATARTVTPKGLPGKAPPRKAGVSPSFLTKKAREPPREPRE 155

QY 62 FRPPTTPEHYMLSYRTLSADARKGNSSVKLEAGLANITTSFDKODRGCPVVRKOR 121
156 FRPPTTPEHYMLSYRTLSADARKGNSSVKLEAGLANITTSFDKODRGCPVVRKOR 215
QY 122 YFEDISALEKDGILGAEIRILTRKKRSPDAPKAPGGRAPGKLSKSCPSGRQPSLIDVR 181
216 YFEDISALEKDGILGAEIRILTRKKRSPDAPKAPGGRAPGKLSKSCPSGRQPSLIDVR 275
QY 182 SVPGIDSGMVEYFDIMKLFERNKNSAQCLLEEMERAVDGLGIDRRAQVHKAL 241
276 SVPGIDSGMVEYFDIMKLFERNKNSAQCLLEEMERAVDGLGIDRRAQVHKAL 335
QY 242 FLYFGRTRKRDLEFEIRKASGODKTYEYLFQSRKRRAPLARTROGKRRSKMLKARCS 301
336 FLYFGRTRKRDLEFEIRKASGODKTYEYLFQSRKRRAPLARTROGKRRSKMLKARCS 395
QY 302 KRALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPEST 361
396 KRALHVNFKDMGMDWIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPEST 455
QY 362 PPTCCVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 401
456 PPTCCVPTRLSPISILFIDSANNVYKQYEDMNVESGCR 495
Db

RESULT 6
US-09-730-772-14
Sequence 14, Application US/09730772
Patent No. US2001001131A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730.772
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836.081
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-730-772-14

Query Match 42.3%; Score 903; DB 9; Length 436;
Best Local Similarity 44.9%; Pred. No. 56-66;
Matches 200; Conservative 62; Mismatches 109; Indels 74; Gaps 14;
QY 7 KPGHPOTQATRRATYTPRGOLPGGKAPPKASVSSFLTKARPPPPREKPPPP 66
16 KEGRMP---RAPRENATAREPLDRQPPPPRPPPP-----QRRPPQPPAREPPGRPR 66
QY 67 ITPHEYMLSYRTLSADARKGNSSVKLEAGLANITTSFDKODRGCPV---VRRORYFD 125
67 LVPHEYMLSYRTLSADARKGNSSVKLEAGLANITTSFDKODRGCPV---VRRORYFD 126
QY 126 ISAL-ERDGLGAEIRILTRKKRSPDAPKAPGGRAPGKLSKSCPSGRQPSLIDVNSVP 184
127 VSTLSKREELVAGADVLFQAPALAPPA---APLALRLPVAAPAGS-----AEP 175
QY 185 GLDGS---GMEYFDIMKLFERNKNSAQCLLELE-AM-ERGRA-----VDL 224
176 GPAGAPRPPMVEYFDIMKLFERNKNSAQCLLELE-AM-ERGRA-----VDL 234
QY 225 RGLGFDRAAROVHEKALFLVFGTRKRDLEFEIRKAR-----261
235 RSLGFGRRRTPOERALLVFSRSQKTL-FAEMREQLGSATEVYVGGGAGSGPPPP 293
QY 262 ----SGODKTYEYLFQSRKRRAPLARTROGKRRSKMLKARCSKALHVNFKDMGMD 316
294 PPPPGTDPDAGIMSP---SPGRRRRTAFASRGKRRGKSRKRLKALHVNFKELGMD 351
QY 317 WIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISI 376
352 WIIAPLEYEAFHCEGLCEPPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISI 411
QY 377 LFTDSANNVYKQYEDMNVESGCR 401
412 LFTDSANNVYKQYEDMNVESGCR 436
Db

RESULT 7
US-09-735-849-14
Sequence 14, Application US/09735849
Patent No. US20010037017A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/735.849
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836.081
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176
 TELE: 619-235-0176
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 436 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-735-849-14

Query Match 42.3%; Score 903; DB 9; Length 436;
 Best Local Similarity 44.9%; Pred. No. 5e-66;

Matches 200; Conservative 62; Mismatches 109; Indels 74; Gaps 14;

DB 7 KRGHPQTRQATFATFVPGKQLPGKAPKAGSVSSFLKKARPPREPPREPPPP 66
 16 KEGRRP---RAPRENAATAREPLDRQPPPPROEP-----QRRPPQPPAREPPRGPR 66
 QY 67 TTPHEYMLSLYRTSLDADRKGNSSVKLEAGLANTITSFIDKGDGRGPV-VKQRYVFD 125
 DB 67 LVPHEYMLSLYRTSLDADRKGNSSVKLEAGLANTITSFIDKGDGRGPV-VKQRYVFD 126
 QY 126 ISAL-EXDGLGAEIRIRKKRPSDTAKPAPGGGAAQLKSSCPSSGQAPSLDVRVSP 184
 DB 127 VSTLSDKKELVGADVRLFRQAPALAPPA--APLALRLVAPAAAGS-----AP 175
 QY 185 GLDGS---GWEYFDIMKLFNFKNSAQCLLELE-AM--ERGRA-----VDL 224
 DB 176 GPAGAPRRGWEYFDVWRGRP-QPMKQCLLELRAMGEPGADEARPPQOQPPRPL 234
 QY 225 RGLGDPRAQVHEKALFLVFGTKRKDLFENETAR----- 261
 DB 225 RSLGGRVYRTPQERALLVFEFSRSQKTVL-FAEMREQLGSATEVVGPGGAGSGPPPP 293
 QY 262 -----SGDDKTYEYLFESQRRRRAPLATRQGRKPSKYLKARCSKRLAHVFKMGMD 316
 DB 294 PPPPSGPPDAGLWSP--SPGRRRTAPASRGRKRGKSRKSCSKPLHVNFKELGMD 351
 QY 317 WIIAPLEYEAFHCEGCEPLRSLHLEPTNHAVIQTLNMSMDPESTPPCTCVPTRLSPISI 376
 DB 352 WIIAPLEYEAFHCEGCEPLRSLHLEPTNHAVIQTLNMSMDPESTPPCTCVPTRLSPISI 411
 QY 377 LFIDSANNVYKQYEDMVESGCR 401
 DB 412 LYIDAGNNVYKQYEDMVESGCR 436

RESULT 8

US-09-945-182-26
 Sequence 26, Application US/09945182
 Patent No. US20020160494A1
 GENERAL INFORMATION:

APPLICANT: Celeste, Anthony J.

Kozney, John

Rosen, Vicki A.

Molman, Neil

Thomsen, Gerald H.

Melton, Douglas A.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/945,182
 FILING DATE: 31-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/808,324
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REGISTRATION NUMBER: 32,618
 REFERENCE/DOCKET NUMBER: 5202-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498-8260
 TELEFAX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-945-182-26

Query Match 36.1%; Score 771; DB 10; Length 321;
 Best Local Similarity 51.1%; Pred. No. 2.3e-55;
 Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

QY 117 VKQRYVFDISAL-EXDGLGAEIRIRKKRPSDTAKPAPGGGAAQL-KLSCPSGQ 173
 DB 9 LKQRYVFDISAL-EXDGLGAEIRIRKKRPSDTAKPAPGGGAAQL-KLSCPSGQ 173
 QY 174 PASLDVRV--PGLDGSWEYFDIMKLFNFKNSAQCLLELE-AM--ERGRA----- 221
 DB 60 -PLLDARTLDQAPAPACWEYFDVWQGLRH-QPMKQCLLELRAMGELDAGEAEARAG 117
 QY 222 -----VDLRGFGPRAAQVHEKALFLVFGTKRKDLFENETARSGDDT----- 268
 DB 118 PQQPPPPDLRSLGFGRRVPPQERALLVFTISQKNTL-FAEMREQLGSATEVVGPGGAGSGPPPP 293
 QY 269 -----YEEYLFESQ-RRRRRAPLATRQGRKPSKYLKARCSKRLAHVFKMGMD 316
 DB 177 GSWPPSGAPDAPRPMPLPSGRRRRRTAPASRGRKRGKSRKSCSKPLHVNFKELGMD 351
 QY 317 WIIAPLEYEAFHCEGCEPLRSLHLEPTNHAVIQTLNMSMDPESTPPCTCVPTRLSPISI 376
 DB 237 WIIAPLEYEAFHCEGCEPLRSLHLEPTNHAVIQTLNMSMDPESTPPCTCVPTRLSPISI 411
 QY 377 LFIDSANNVYKQYEDMVESGCR 401
 DB 297 LYIDAGNNVYKQYEDMVESGCR 321

RESULT 9

US-10-188-246-12
 Sequence 12, Application US/10188246
 Publication No. US20030087274A1
 GENERAL INFORMATION:

APPLICANT: Anderson, David W.

APPLICANT: Boldog, Ferenc

APPLICANT: Casman, Stacie

APPLICANT: Edinger, Shlomil

APPLICANT: Gerlach, Valerie

APPLICANT: Gorman, Linda

APPLICANT: Li, Li

APPLICANT: Malynkar, Uriel

APPLICANT: Patlurajan, Meera

APPLICANT: Peymen, John

APPLICANT: Shenoy, Suresh

APPLICANT: Shinkets, Richard

APPLICANT: Vernet, Corine A. M.

APPLICANT: Voss, Edward

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND MET

FILE REFERENCE: 21402-397B US

Thu Aug 28 08:27:33 2003

us-09-901-556c-3.rapb

Page 6

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; CURRENT APPLICATION NUMBER: US/10/188,246
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/303046
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/304502
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/305011
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/306085
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 60/306981
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/360923
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/363636
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/373063
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Custom
; SEQ ID NO: 12
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-246-12

Query Match
Best Local Similarity 35.3%; Score 752.5; DB 15; Length 450;
Matches 170; Conservative 62; Mismatches 124; Indels 59; Gaps 11;

27 QLPGGKAPPKAGSVSSFLKARPPPPREPPPPPTTTPHYMLSTRTSDADRK 86
55 QAAGAAVAF-AAAVPRARARAAAGSG-----FRNGSVVPHFMMSILRLSGARA 105
87 GGNSSVKLEAGLANTITSTFDKQDDRCGPVYRKQVYRDISAL-EKQDLGAELRIIRKK 145
106 GAAAVASAGHGADVTITGTDATQDESAETGQSFILVDSLNADAVGAELRLVRG 165
146 PSDTAPPAAPGGGAAQ-ILKSSCSGKRPASLLDVRSVPGDGSQVTFDITWLFRRFK 204
166 SPT---SGGWSPTSPPLILSTCGAARAPRLISRAEPLVGGWELFDVADMRHR 221
205 NSAQ---LCLEAVERGAV-----DIRGLQF--DRAAQVHKALFLVFGRTK 249
222 REPRPPAFCLL-----RAVAGVPVSPFLALRLQFGMPGGGSAAEERAVLYVSRIO 275
250 KRDLFENEIKARS-----GDDKTYEYELFSQRRRRAPLATR----- 287
276 RKESLFEIRAOARALGALASEPLDPDGTGTASPRAVIGRRRRRTALAGRTAAGSGC 335
288 -QGRRPSKILKACSRKALAHVNFKMGNDMTIAPLEYEAFHCEGCEPPLRSHLEPTNH 346
336 GAGGAGRGRRSRCSRKPLHVDYRKELEMDMTIAPLEYEAFHCEGCEPPLRSHLEPTNH 395
347 AVIQTLMNSMDPESTPTCCVPTRLSPISILFTDSANNVYKYEEDMVVYESGCCR 401
396 AIIQTLMNSAPDAAPASCVPARLSPISILYIDANNVYKYEEDMVVYESGCCR 450

RESULT 10
US-09-945-182-4
; Sequence 4, Application US/09945182
; Patent No. US20020160494A1
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; WOZNEY, JOHN A.
; ROSEN, VICKI A.
; MOLTAN, NEIL A.
; THOMSEN, GERALD H.
; MELTON, DOUGLAS A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:

```

```

ADDRESSER: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182.
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,324
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-945-182-4

Query Match
Best Local Similarity 30.8%; Score 658; DB 10; Length 120;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

282 APLATRGKRPSSKILKACSRKALAHVNFKMGNDMTIAPLEYEAFHCEGCEPPLRSHL 341
1 APLATRGKRPSSKILKACSRKALAHVNFKMGNDMTIAPLEYEAFHCEGCEPPLRSHL 60
342 EPTNAVIQTLMNSMDPESTPTCCVPTRLSPISILFTDSANNVYKYEEDMVVYESGCCR 401
61 EPTNAVIQTLMNSMDPESTPTCCVPTRLSPISILFTDSANNVYKYEEDMVVYESGCCR 120

RESULT 11
US-09-945-182-34
; Sequence 34, Application US/09945182
; Patent No. US20020160494A1
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; WOZNEY, JOHN A.
; ROSEN, VICKI A.
; MOLTAN, NEIL A.
; THOMSEN, GERALD H.
; MELTON, DOUGLAS A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENETICS INSTITUTE, INC.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

```

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,459A
FILING DATE: 09-DEC-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01062
FILING DATE: 19-APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP7/322403
FILING DATE: 17-NOV-1995
PRIORITY APPLICATION DATA: JP7/93664
FILING DATE: 19-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MOSERLIAN
REGISTRATION NUMBER: 19,693
REFERENCE/DOCKET NUMBER: 146,1275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: LINEAR
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
ORGANISM SOURCE:
ORGANISM: HOMOSAPIENS
TISSUE TYPE: FETUS
FEATURE:
NAME/KEY: MP52
LOCATION: 383 TO 501
US-08-945-459A-1

Query Match 30.7%; Score 654; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 2,7e-46;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 283 PLATROGRPSKRNILKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCEGICEPPLRSHE 342
1 PLATROGRPSKRNILKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCEGICEPPLRSHE 60
OY 343 PTNHAVIOTLMSNDPESTPTCCVPTRLSPISILFTIDSANNNVYKQYEDMAYVESCGR 401
61 PTNHAVIOTLMSNDPESTPTCCVPTRLSPISILFTIDSANNNVYKQYEDMAYVESCGR 119

DB 61 PTNHAVIOTLMSNDPESTPTCCVPTRLSPISILFTIDSANNNVYKQYEDMAYVESCGR 119

RESULT 14
US-09-068-253-2
Sequence 2, Application US/09068253
Patent No. US20020168381A1
GENERAL INFORMATION:
APPLICANT: SHIMURA, Takesada
APPLICANT: TORIYAMA, Satsuki
TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
FILE REFERENCE: 146,1286
CURRENT APPLICATION NUMBER: US/09/068,253
PRIORITY FILING DATE: 1998-06-09
PRIORITY APPLICATION NUMBER: PCT/JP96/03333
PRIORITY FILING DATE: 1996-11-14
PRIORITY APPLICATION NUMBER: JP 7/322402
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens

US-09-068-253-2
Query Match 30.7%; Score 654; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 2,7e-46;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 283 PLATROGRPSKRNILKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCEGICEPPLRSHE 342
1 PLATROGRPSKRNILKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCEGICEPPLRSHE 60
OY 343 PTNHAVIOTLMSNDPESTPTCCVPTRLSPISILFTIDSANNNVYKQYEDMAYVESCGR 401
61 PTNHAVIOTLMSNDPESTPTCCVPTRLSPISILFTIDSANNNVYKQYEDMAYVESCGR 119

DB 61 PTNHAVIOTLMSNDPESTPTCCVPTRLSPISILFTIDSANNNVYKQYEDMAYVESCGR 119

RESULT 15
US-09-880-708-13
Sequence 13, Application US/09880708
Patent No. US20020165361A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121-2189
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,708
FILING DATE: 12-Jun-2001
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/145,060
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Hallie, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 619/677-1465
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-5
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-880-708-13

Query Match 30.4%; Score 649; DB 10; Length 119;
Best Local Similarity 99.2%; Pred. No. 6,8e-46;
Matches 118; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 283 PLATROGRPSKRNILKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCEGICEPPLRSHE 342
1 PLATROGRPSKRNILKARCSRKALHVNFKDMGMDWIIAPLEYEAFHCEGICEPPLRSHE 60
OY 343 PTNHAVIOTLMSNDPESTPTCCVPTRLSPISILFTIDSANNNVYKQYEDMAYVESCGR 401
61 PTNHAVIOTLMSNDPESTPTCCVPTRLSPISILFTIDSANNNVYKQYEDMAYVESCGR 119

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